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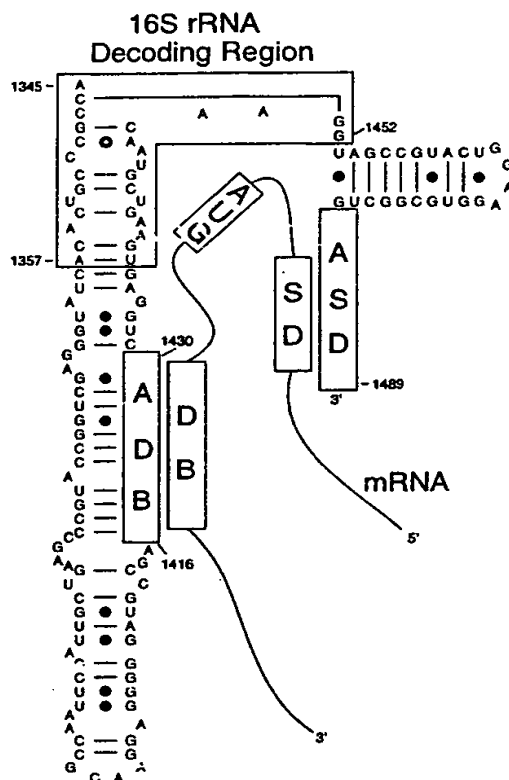


Figure 1A

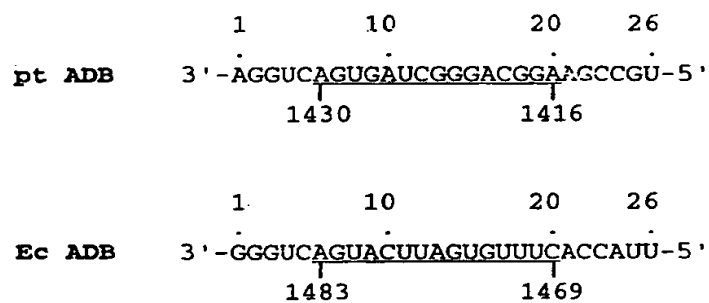


Figure 1B

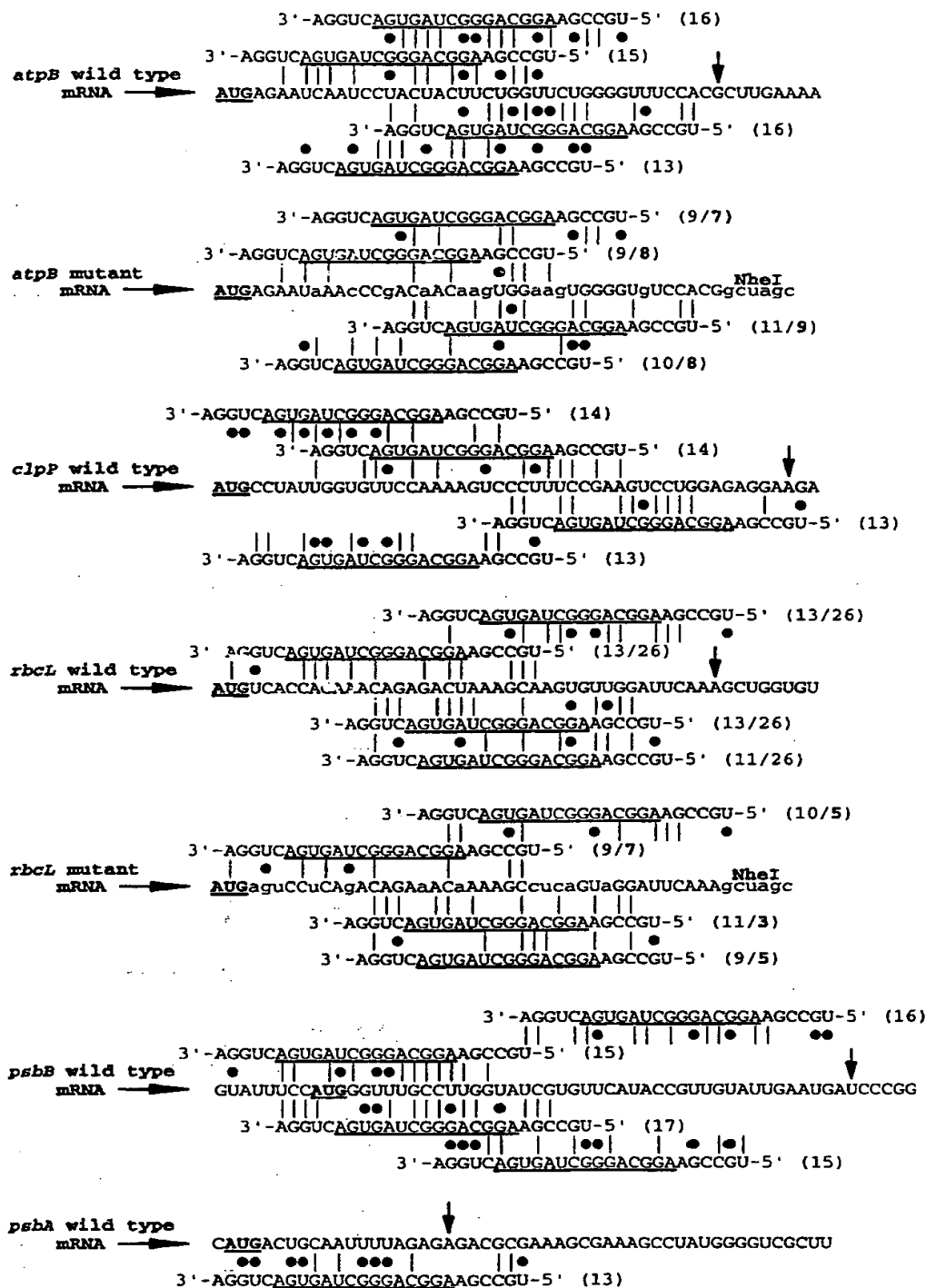


Figure 2A



Figure 2B

PrrnLatpB+DBwt (pHK10)

SacI
 1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG AATTAACCGA
 101 TCGACGTGCa AGCGGACATT TATTTTaaAT TCGATAATTT TTGCAAAAAC
 151 ATTCGACAT ATTTATTTAT TTTATTATTA TGAGAATCAA TCCTACTACT
 NheI
 201 TCTGGTTCTG GGGTTCCAC Ggctagc

PrrnLatpB-DB (pHK11)

SacI
 1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG AATTAACCGA
 101 TCGACGTGCa AGCGGACATT TATTTTaaAT TCGATAATTT TTGCAAAAAC
 NheI
 151 ATTCGACAT ATTTATTTAT TTTATTATTA TGAGAgctag c

PrrnLatpB+DBm (pHK50)

SacI
 1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG AATTAACCGA
 101 TCGACGTGCa AGCGGACATT TATTTTaaAT TCGATAATTT TTGCAAAAAC
 151 ATTCGACAT ATTTATTTAT TTTATTATTA TGAGAAaAA cCCgACaCa
 NheI
 201 agTGGaagTG GGGTgTCCAC Ggctagc

PrrnLclpP+DBwt (pHK12)

SacI
 1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TTACGTTTCC
 101 ACCTCAAAGT GAAATATAGT ATTTAGTTCT TTCTTTCATT TAATGCCTAT
 NheI
 151 TGGTGTTCa AAAGTCCCTT TCCGAAGTCC TGGAGAGGAA gctagc

PrrnLclpP-DB (pHK13)

SacI
 1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TTACGTTTCC
 NheI
 101 ACCTCAAAGT GAAATATAGT ATTTAGTTCT TTCTTTCATT TAATGCCTgc
 151 tagc

Figure 3A

PrrnLrbcl+DBwt (pHK14)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
101 CTTGTTGTTG TGAAaAATTCT TAATTCATGA GTTGTAGGGA GGGATTTATG
NheI
151 TCACCACAAA CAGAGACTAA AGCAAGTGTT GGATTCAAAG ctagc

PrrnLrbcl-DB (pHK15)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
101 CTTGTTGTTG TGAAaAATTCT TAATTCATGA GTTGTAGGGA GGGATTTATG
NheI
151 TCAGctagc

PrrnLrbcl+DBm (pHK54)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
101 CTTGTTGTTG TGAAaAATTCT TAATTCATGA GTTGTAGGGA GGGATTTATG
NheI
151 aguCCuCAgA CAGAAaCaAA AGCcucaGTa GGATTCAAAG ctagc

PrrnLpsbB+DBwt (pHK16)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG CAATGCAATA
101 AAGTTACGTA GTGTCTATTT ATCTTTGATA TAAGGGGTAT TTCCATGGGT
NheI
151 TTGCCTTGGT ATCGTGTTCA TACCGTTGTA TTGAATGATg ctagc

PrrnLpsbB-DB (pHK17)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG CAATGCAATA
NcoI NheI
101 AAGTTACGTA GTGTCTATTT ATCTTTGATA TAAGGGGTAT TTccatggct
151 agc

Figure 3B

PrnLpsbA+DBwt (pHK21)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAA AAAAGCCTTC
101 CATTTTCTAT TTTGATTTGT AGAAACTAG TGTGCTTGGG AGTCCCTGAT
NheI
151 GATTAAATAA ACCAAGATTT TACCATGACT GCAATTTTAG AGAGagctag
201 c

PrnLpsbA-DB (pHK22)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAA AAAAGCCTTC
101 CATTTTCTAT TTTGATTTGT AGAAACTAG TGTGCTTGGG AGTCCCTGAT
NcoI NheI
151 GATTAAATAA ACCAAGATTT TAccatggct agc

PrnLpsbA-DB(+GC) (pHK23)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG CAAAAGCCT
101 TCCATTTTCT ATTTTGATTT GTAGAAACT AGTGTGCTTG GGAGTCCCTG
NcoI NheI
151 ATGATTAAAT AAACCAAGAT TTTAccatgg ctacg

Figure 3C

PrrnLT7g10+DB/Ec (pHK18)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG GGAGACCACA
101 ACGGTTTCCC aCTAGAAATA ATTTTGTTTA ACTTTAAGAA GGAGATATAC
NheI
151 ATATGGCaAG CATGACTGGT GGACAGgcta gc

PrrnLT7g10+DB/pt (pHK19)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG GGAGACCACA
101 ACGGTTTCCC aCTAGAAATA ATTTTGTTTA ACTTTAAGAA GGAGATATAC
NheI
151 ATATGGCaAt cactagccct gccttGgcta gc

PrrnLT7g10-DB (pHK20)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG GGAGACCACA
101 ACGGTTTCCC aCTAGAAATA ATTTTGTTTA ACTTTAAGAA GGAGATATAC
NheI
151 ATATGgctag c

Figure 3D

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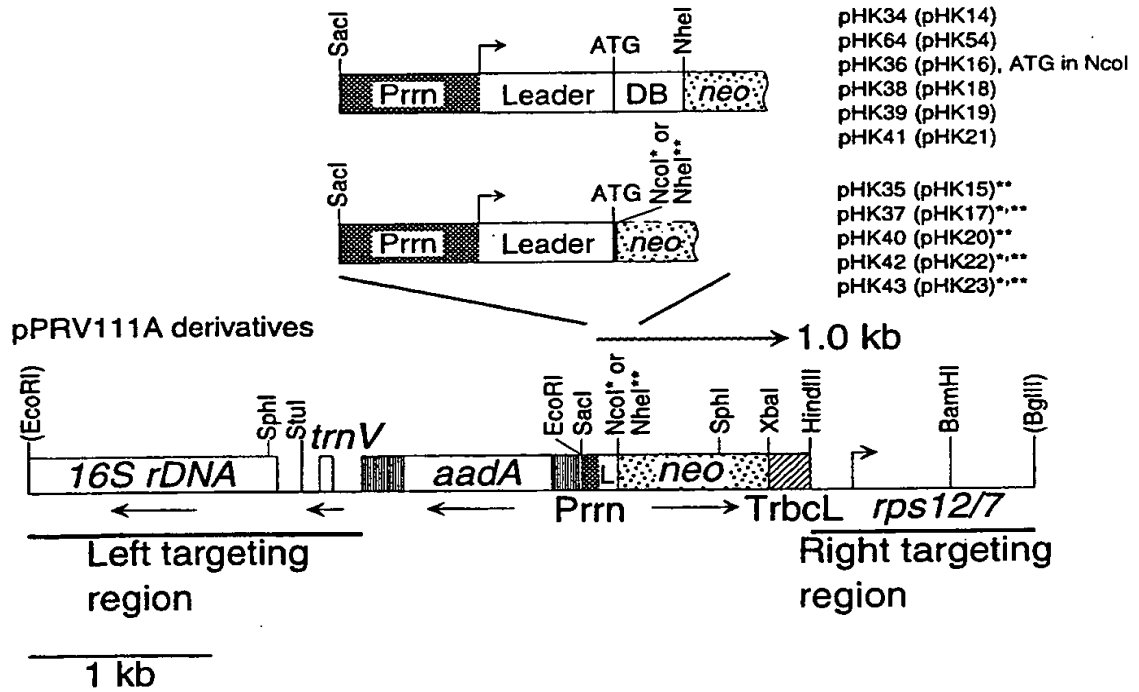


Figure 4A

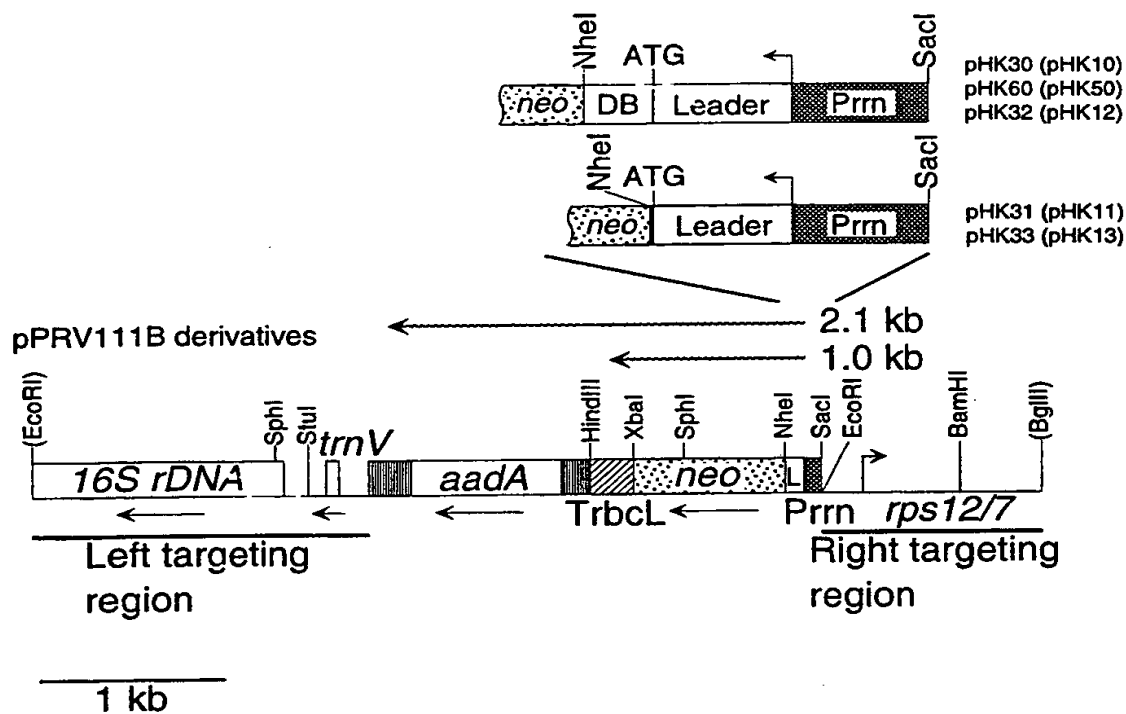
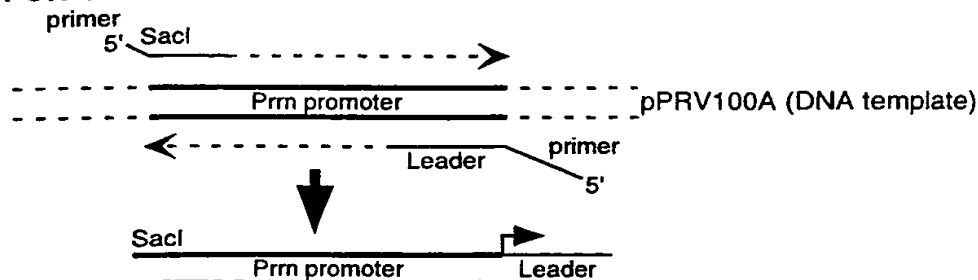
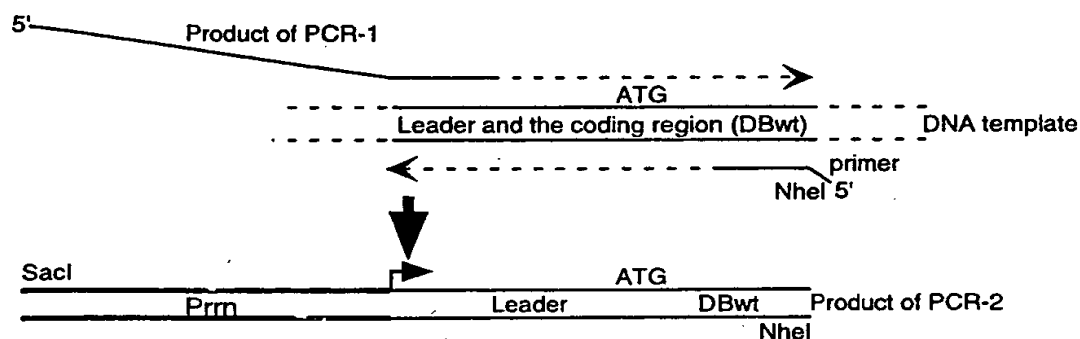
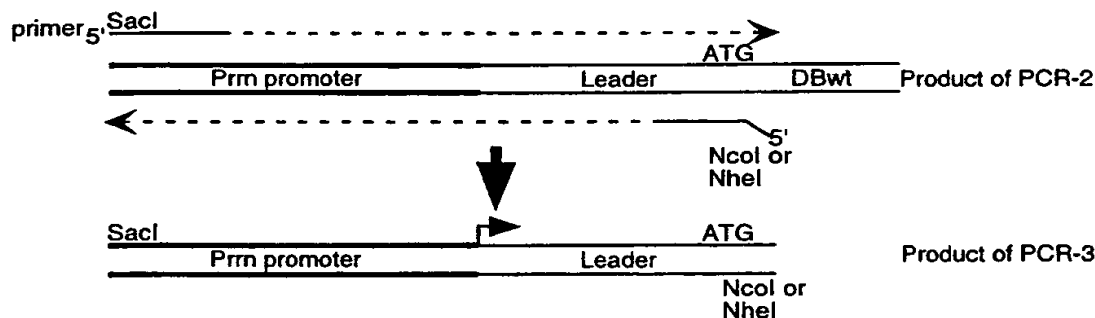
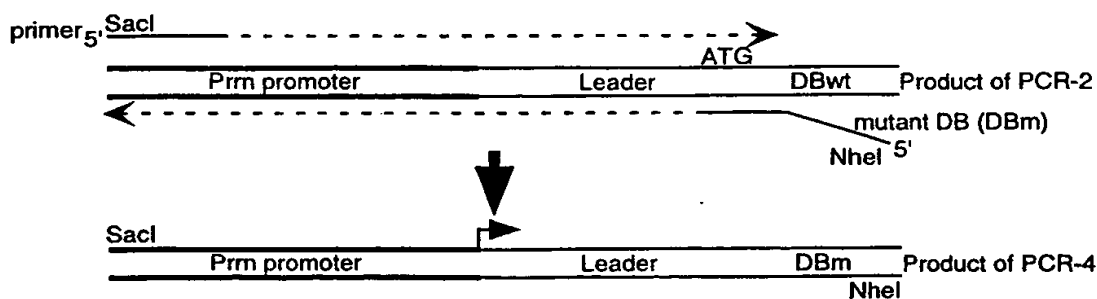


Figure 4B

PCR-1**PCR-2: Construct with wild-type DB (DBwt)****PCR-3: Construct without DB****PCR-4: Construct with mutant DB (DBm)****Figure 5**

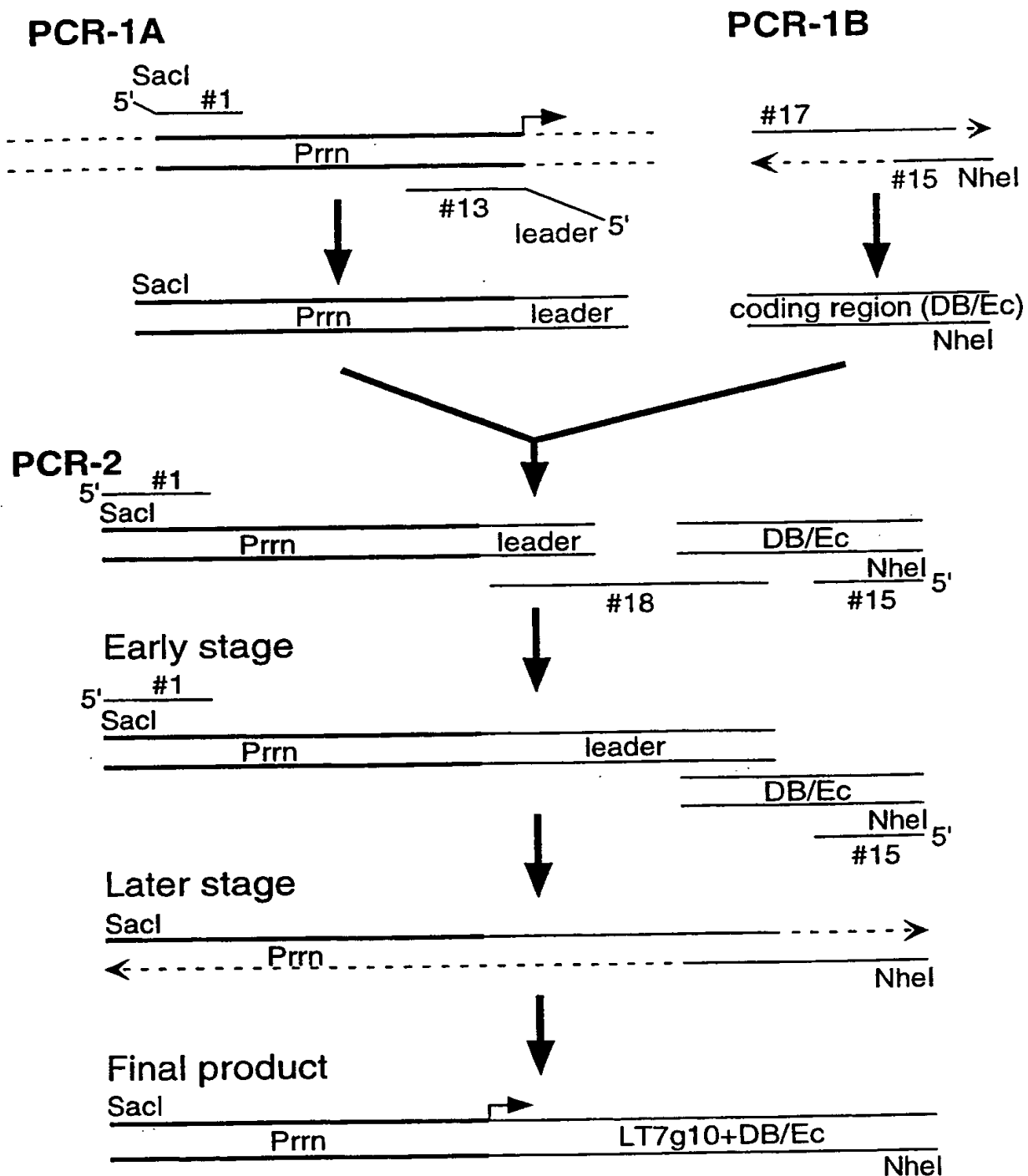
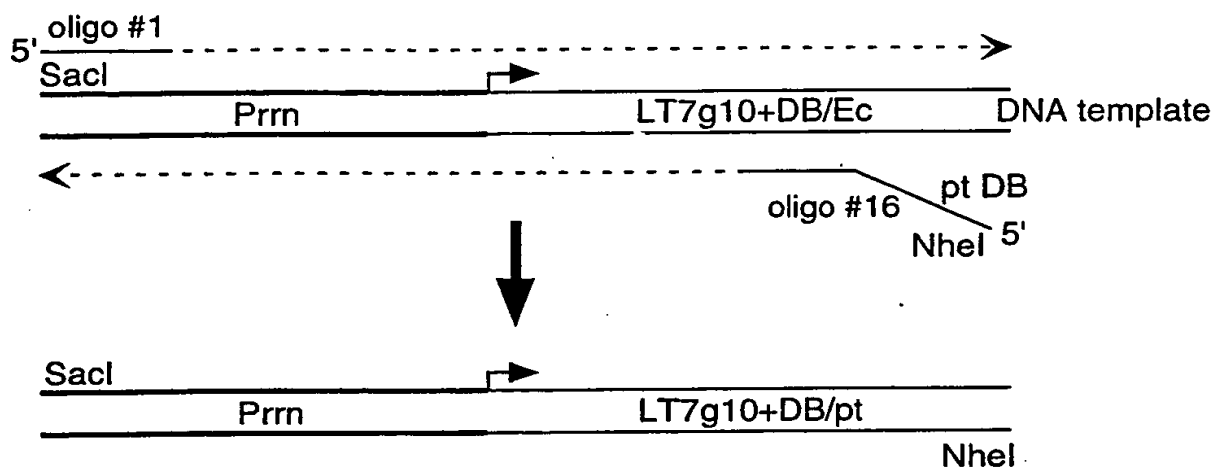


Figure 6

**Figure 7**

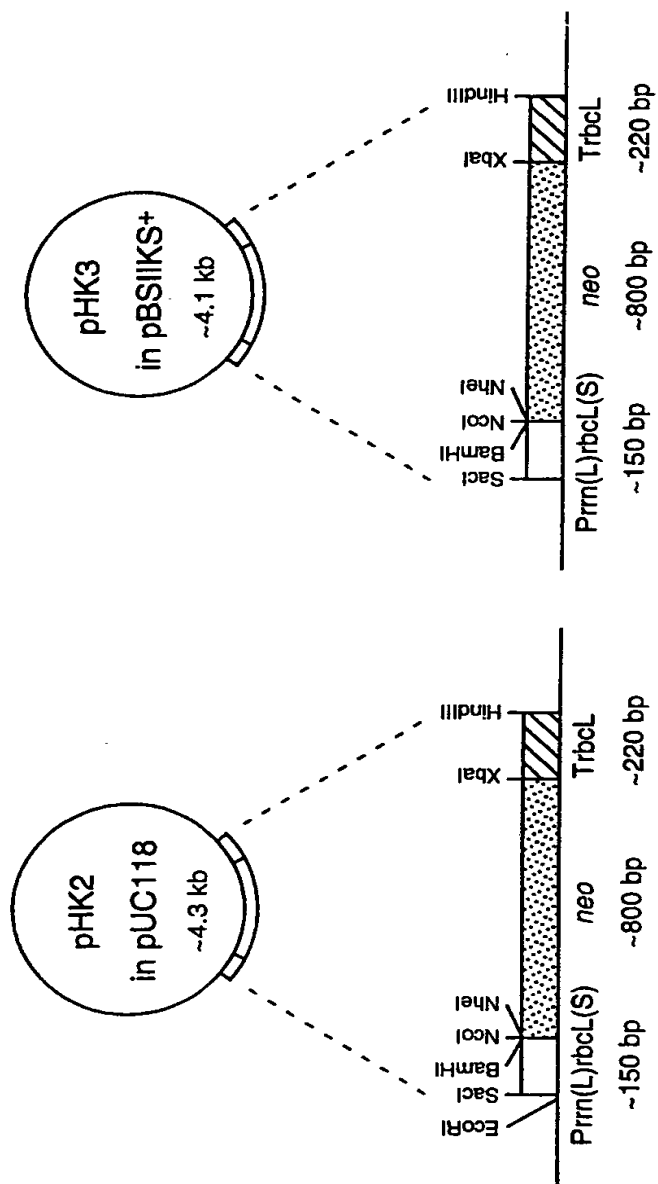


Figure 8

1 SacI
 gagctcggta cccaaaGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG
 51 AGGCTCGTGG GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG
 101 CGAACTCCGG GCGAATAcGA AGCGcTtGGA TACAGTTGTA GGGAGGGATc NcoI
 NheI
 151 catggctagc ATTGAACAAG ATGGATTGCA CGCAGGTTCT CCGGCCGCTT
 201 GGGTGGAGAG GCTATTTCGGC TATGACTGGG CACAACAGAC AATCGGCTGC
 251 TCTGATGCCG CCGTGTTCCTG GCTGTCAGCG CAGGGGCGCC CGGTTCTTTT
 301 TGTCAAGACC GACCTGTCCG GTGCCCTGAA TGAAGTCCAG GACGAGGCAG
 351 CGCGGCTATC GTGGCTGGCC ACGACGGGCG TTCCTTGCGC AGCTGTGCTC
 401 GACGTTGTCA CTGAAGCGGG AAGGGACTGG CTGCTATTGG GCGAAGTGCC
 451 GGGGCAGGAT CTCCTGTCAT CTCACCTTGC TCCTGCCGAG AAAGTATCCA
 501 TCATGGCTGA TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC
 551 CCATTCGACC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT
 601 GGAAGCCGGT CTTGTTCGATC AGGATGATCT GGACGAAGAG CATCAGGGGC
 651 TCGCGCCAGC CGAACTGTTC GCCAGGCTCA AGGCGCGCAT GCCCGACGGC
 701 GAGGATCTCG TCGTGACACA TGGCGATGCC TGCTTGCCGA ATATCATGGT
 751 GGAAAATGGC CGCTTTTCTG GATTCATCGA CTGTGGCCGG CTGGGTGTGG
 801 CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT TGCTGAAGAG
 851 CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTACG GTATCGCCGC
 901 TCCCGATTCTG CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTCT
 XbaI
 951 GAgcgggtct agagtAGACA TTAGCAGATA AATTAGCAGG AAATAAAGAA
 1001 GGATAAGGAG AAAGAACTCA AGTAATTATC CTTCGTTCTC TTAATTGAAT
 1051 TGCAATTAAA CTCGGCCCAA TCTTTTACTA AAAGGATTGA GCCGAATACA
 1101 ACAAAGATTC TATTGCATAT ATTTTGAATA AGTATATACT TACCTAGATA
 HindIII
 1151 TACAAGATTT GAAATACAAA ATCTAGcaag ctt

Figure 9

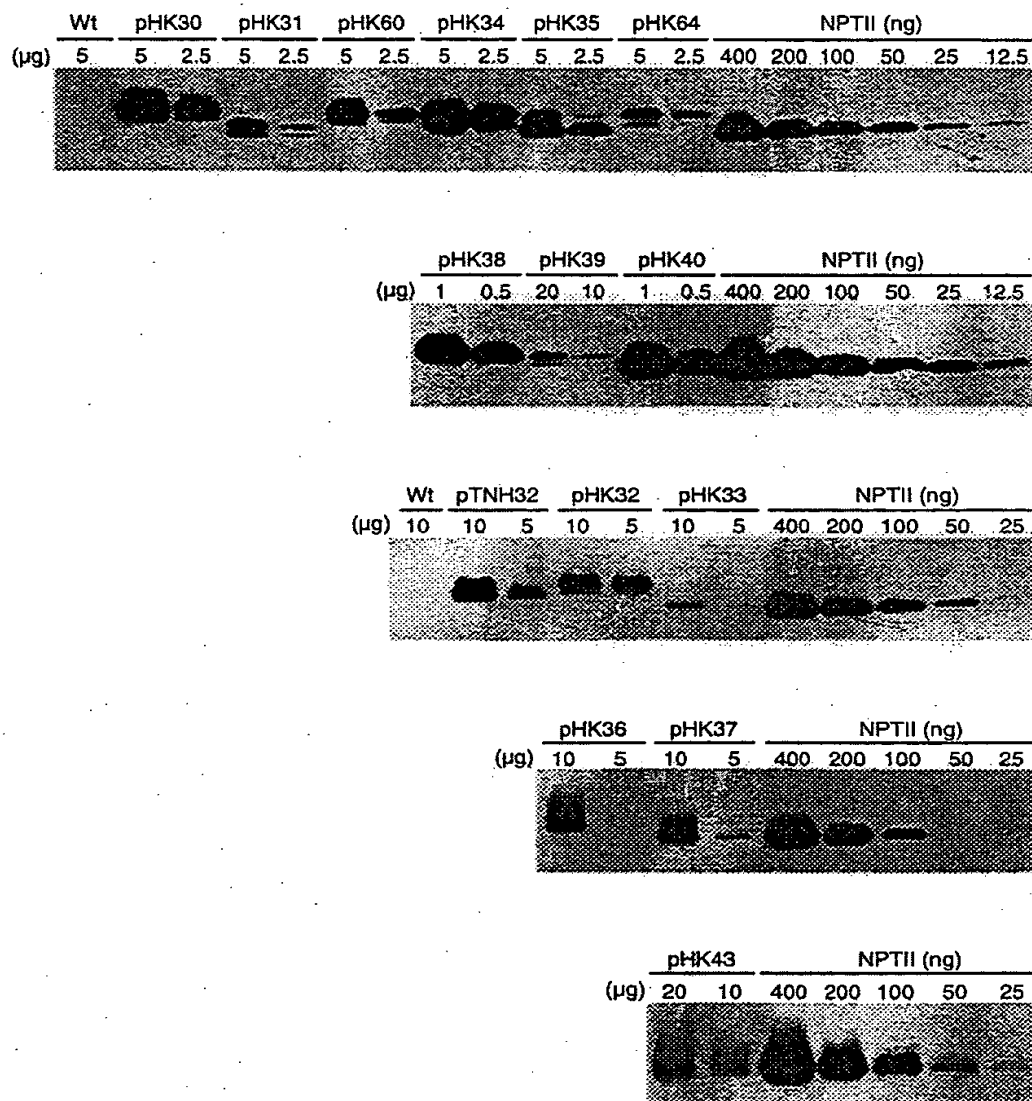


Figure 10

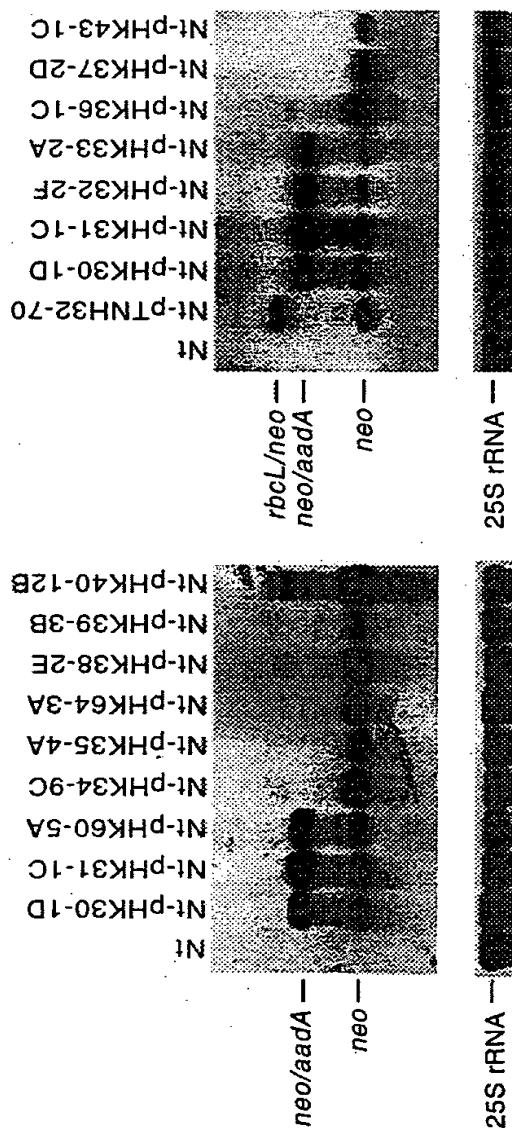


Figure 11

atpB wt	AUG	AGA	AUC	AAU	CCU	ACU	ACU	ACU	UCU	GGU	UCU	GGG	GUU	UCC	ACG
	Met	Arg	Ile	Asn	Pro	Thr	Thr	Thr	Ser	Gly	Ser	Gly	Val	Ser	Thr
	1.0	0.22	0.27	0.61	0.30	0.37	0.37	0.31	0.38	0.31	0.38	0.26	0.35	0.14	0.15
Triplet/1000	24.6	7.8	15.5	18.1	13.5	18.4	18.4	20.2	28.2	20.2	19.2	24.9	9.1	7.5	
atpB m	AUG	AGA	AUA	AAC	CCG	ACA	ACA	AGU	Gga	AGU	GGG	GUG	UCC	ACG	
	Met	Arg	Ile	Asn	Pro	Thr	Thr	Ser	Gly	Ser	Gly	Val	Ser	Thr	
	1.0	0.22	0.29	0.39	0.30	0.23	0.23	0.14	0.24	0.14	0.26	0.21	0.14	0.15	
Triplet/1000	24.6	7.8	16.6	11.4	13.2	11.7	11.7	9.3	17.9	9.3	19.2	15.3	9.1	7.5	
rbcL wt	AUG	UCA	CCA	CAA	ACA	GAG	ACU	AAA	GCA	AGU	GUU	GGA	UUC	AAA	
	Met	Ser	Pro	Gln	Thr	Glu	Thr	Lys	Ala	Ser	Val	Gly	Phe	Lys	
	1.0	0.21	0.24	0.57	0.23	0.38	0.37	0.60	0.29	0.14	0.35	0.24	0.40	0.60	
Triplet/1000	24.6	13.5	10.6	21.0	11.7	12.4	18.4	22.0	18.1	9.3	24.9	17.9	22.5	22.0	
rbcL m	AUG	agu	CCU	CAG	ACA	GAA	ACA	AAA	GCC	uca	GUA	GGA	UUC	AAA	
	Met	Ser	Pro	Gln	Thr	Glu	Thr	Lys	Ala	Ser	Val	Gly	Phe	Lys	
	1.0	0.14	0.30	0.43	0.23	0.62	0.23	0.60	0.16	0.21	0.31	0.24	0.40	0.60	
Triplet/1000	24.6	9.3	13.5	15.5	11.7	20.7	11.7	22.0	10.1	13.5	21.8	17.9	22.5	22.0	
T7gl0+DB/EC	AUG	GCa	AGC	AUG	ACU	GGU	GGA	CAG	gcu	agc	auu	gaa	caa	gaa	
	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Ala	Ser	Ile	Glu	Gln	Asp	
	1.0	0.29	0.07	1.00	0.37	0.38	0.24	0.43	0.39	0.07	0.45	0.62	0.57	0.75	
Triplet/1000	24.6	18.1	4.7	24.6	18.4	28.2	17.9	15.5	24.4	4.7	25.9	20.7	21.0	24.6	
T7gl0+DB/pt	AUG	GCa	Auc	acu	agc	ccu	gcc	uug	gcu	agc	auu	gaa	caa	gaa	
	Met	Ala	Ile	Thr	Ser	Pro	Ala	Leu	Ala	Ser	Ile	Glu	Gln	Asp	
	1.0	0.29	0.27	0.37	0.07	0.30	0.16	0.24	0.39	0.07	0.45	0.62	0.57	0.75	
Triplet/1000	24.6	18.1	15.5	18.4	4.7	13.5	10.1	34.7	24.4	4.7	25.9	20.7	21.0	24.6	
T7gl0-DB	AUG	gcu	agc	auu	gaa	caa	gaa	gga	uug	cac	gca	ggu	ucu	ccg	
	Met	Ala	Ser	Ile	Glu	Gln	Asp	Gly	Leu	His	Ala	Gly	Ser	Pro	
	1.0	0.39	0.07	0.45	0.62	0.57	0.75	0.24	0.24	0.28	0.29	0.38	0.31	0.30	
Triplet/1000	24.6	24.4	4.7	25.9	20.7	21.0	24.6	17.9	34.7	9.1	18.1	28.2	20.2	13.2	

Figure 12

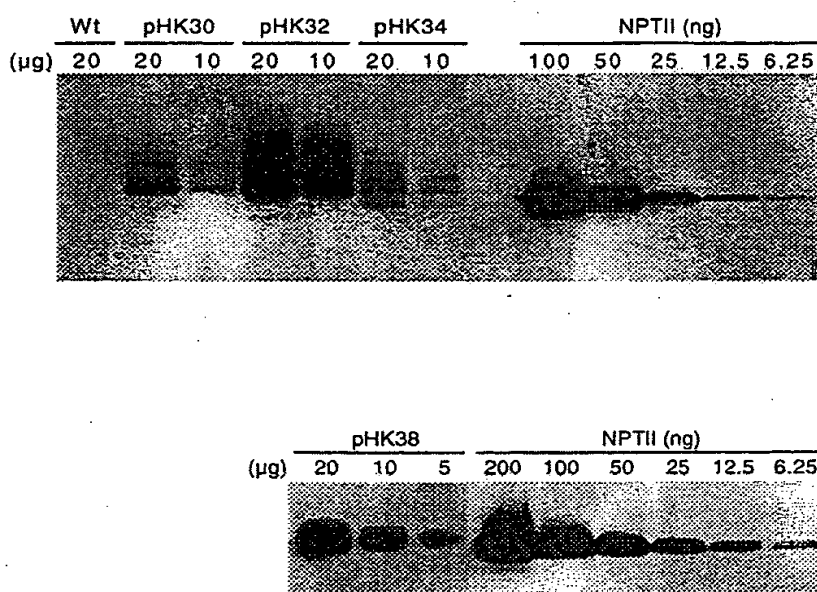


Figure 13A

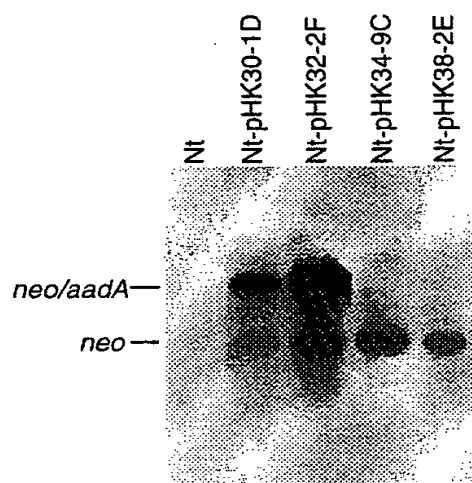


Figure 13B

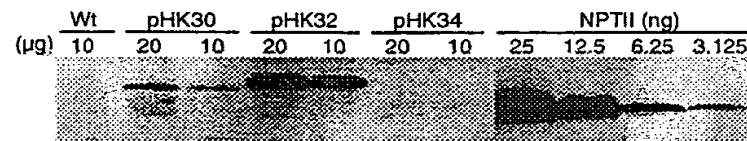


Figure 14

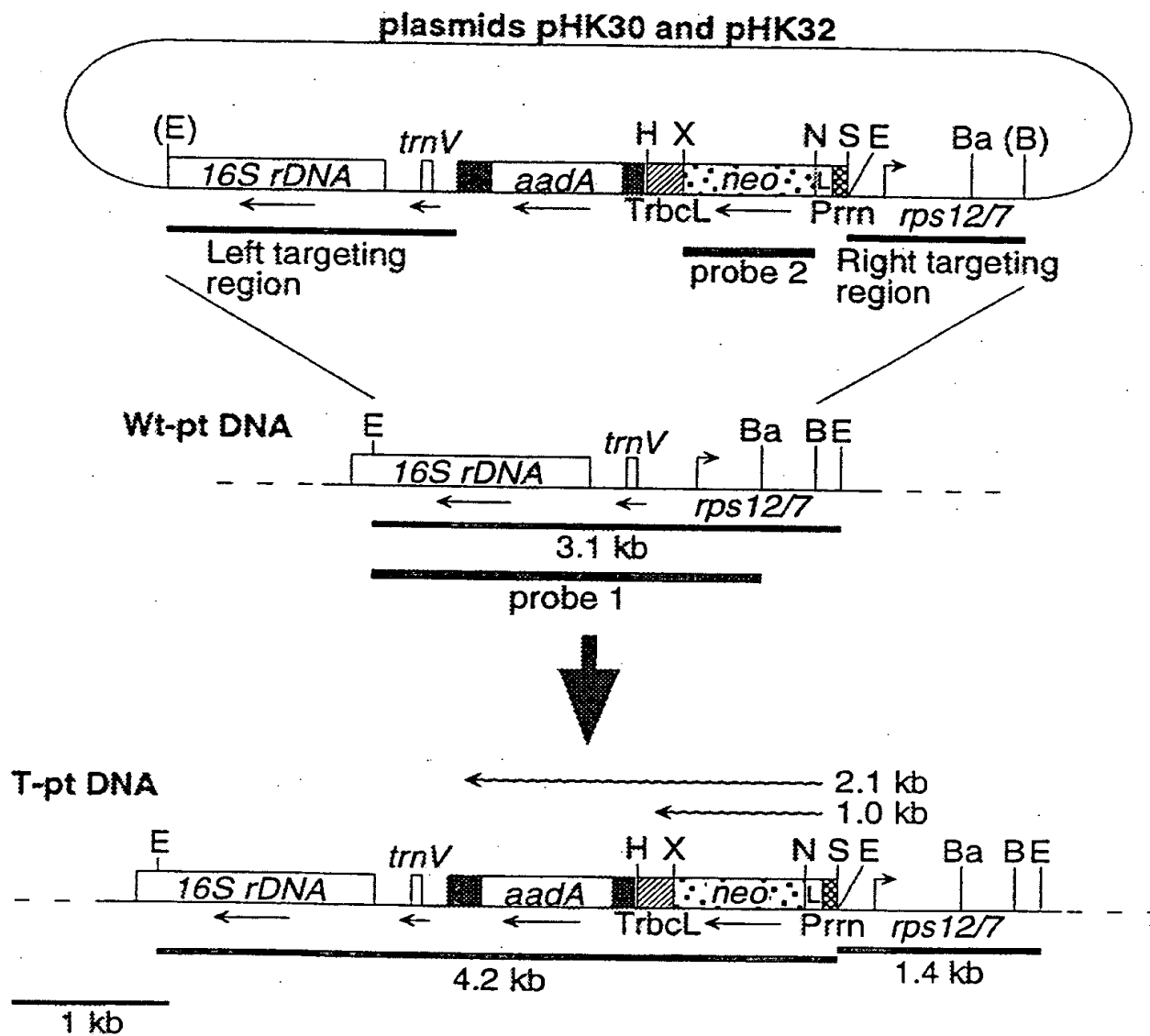


Figure 15A

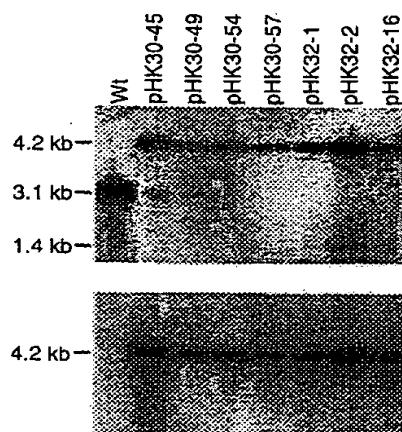


Figure 15B

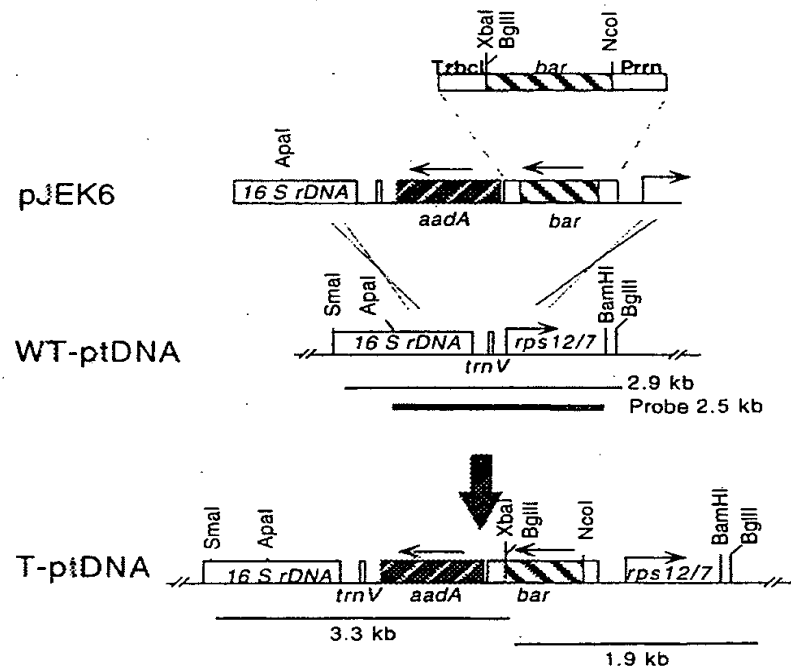


Figure 16A

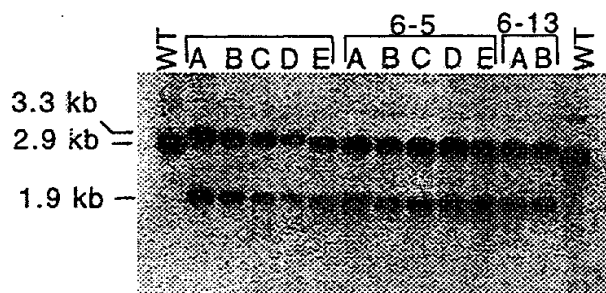


Figure 16B

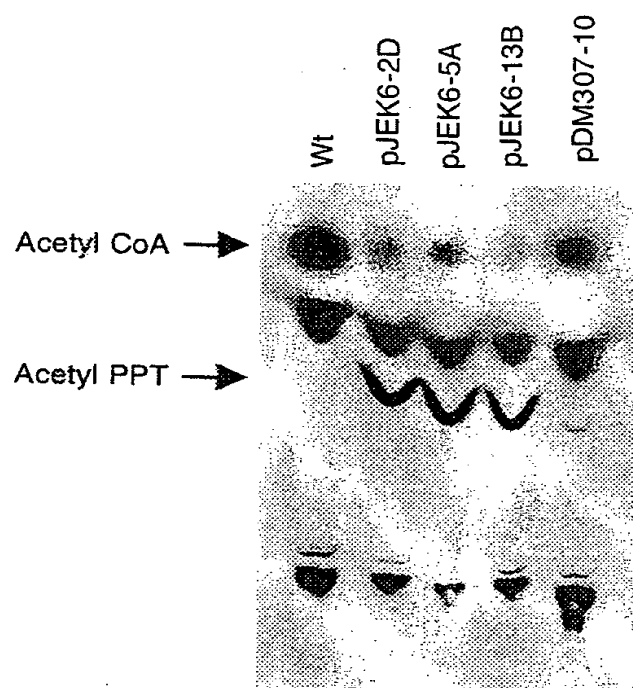


Figure 17

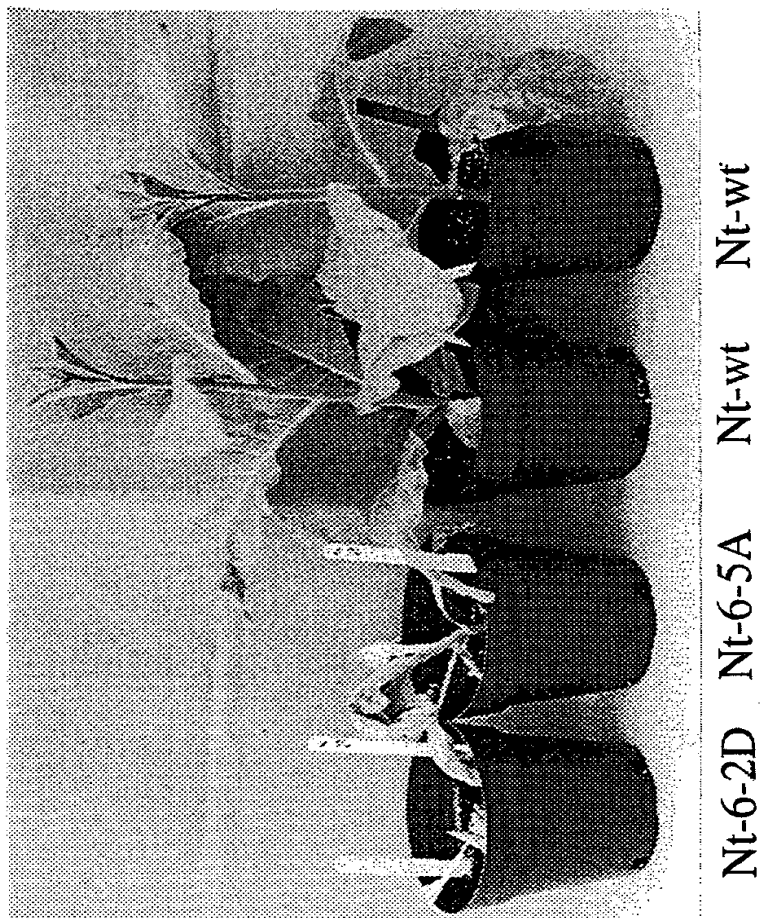


Figure 18A

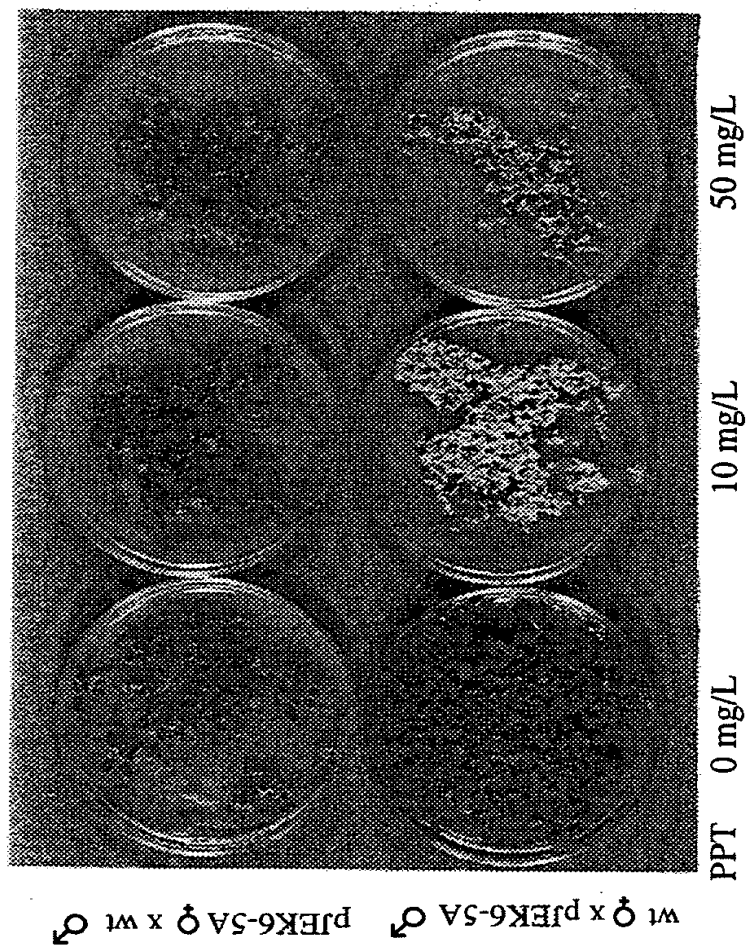


Figure 18B

NcoI

CCATGGcaccacaaacagagAGCCCAGAACGACGCCCGCCGACATCCGCCGTGCCACCG
 -----+-----+-----+-----+-----+-----+ 60
 GGTACcgtggtgtttgtctcTCGGGTCTTGCTGCGGGCCGGCTGTAGGCGGCACGGTGGC
 M A P Q T E S P E R R P A D I R R A T E

 AGGCGGACATGCCGGCGGTCTGCACCATCGTCAACCACTACATCGAGACAAGCACGGTCA
 -----+-----+-----+-----+-----+-----+ 120
 TCCGCCTGTACGGCCGCCAGACGTGGTAGCAGTTGGTGATGTAGCTCTGTTTCGTGCCAGT
 A D M P A V C T I V N H Y I E T S T V N

 ACTTCCGTACCGAGCCGCAGGAACCGCAGGAGTGGACGGACGACCTCGTCCGTCTGCGGG
 -----+-----+-----+-----+-----+-----+ 180
 TGAAGGCATGGCTCGGCGTCCTTGGCGTCCTCACCTGCCTGCTGGAGCAGGCAGACGCCC
 F R T E P Q E P Q E W T D D L V R L R E

 AGCGCTATCCCTGGCTCGTCGCGGAGGTGGACGGCGAGGTGCGCCGGCATCGCCTACGCGG
 -----+-----+-----+-----+-----+-----+ 240
 TCGCGATAGGGACCGAGCAGCGGCTCCACCTGCCGCTCCAGCGGCCGTAGCGGATGCGCC
 R Y P W L V A E V D G E V A G I A Y A G

 GCCCCTGGAAGGCACGCAACGCCTACGACTGGACGGCCGAGTCGACCGTGTACGTCTCCC
 -----+-----+-----+-----+-----+-----+ 300
 CGGGGACCTTCGTGCGTTGCGGATGCTGACCTGCCGGCTCAGCTGGCACATGCAGAGGG
 P W K A R N A Y D W T A E S T V Y V S P

 CCCGCCACCAGCGGACGGGACTGGGCTCCACGCTCTACACCCACCTGCTGAAGTCCCTGG
 -----+-----+-----+-----+-----+-----+ 360
 GGGCGGTGGTGCCTGCCCTGACCCGAGGTGCGAGATGTGGGTGGACGACTTCAGGGACC
 R H Q R T G L G S T L Y T H L L K S L E

 AGGCACAGGGCTTCAAGAGCGTGGTCGCTGTCATCGGGCTGCCCAACGACCCGAGCGTGC
 -----+-----+-----+-----+-----+-----+ 420
 TCCGTGTCCCGAAGTTCTCGCACCAGCGACAGTAGCCCCGACGGGTTGCTGGGCTCGCAGC
 A Q G F K S V V A V I G L P N D P S V R

 GCATGCACGAGGCGCTCGGATATGCCCCCGCGGCATGCTGCGGGCGGCCGGCTTCAAGC
 -----+-----+-----+-----+-----+-----+ 480
 CGTACGTGCTCCGCGAGCCTATACGGGGGGCGCCGTACGACGCCCGCCGCGCAAGTTCG
 M H E A L G Y A P R G M L R A A G F K H

 ACGGGAAGTGGCATGACGTGGGTTTCTGGCAGCTGGACTTCAGCCTGCCGGTACCGCCCC
 -----+-----+-----+-----+-----+-----+ 540
 TGCCCTTGACCGTACTGCACCCAAAGACCGTCGACCTGAAGTCGGACGGCCATGGCGGGG
 G N W H D V G F W Q L D F S L P V P P R

BglII

GTCCGGTCCTGCCCGTCACCGAGATCTGATGAtcgaattcctgcagcccggggatccac
 -----+-----+-----+-----+-----+-----+ 600
 CAGGCCAGGACGGGACGTGGCTCTAGACTACTagcttaaggacgtcgggccccctaggtg
 P V L P V T E I *

XbaI

tagttctaga
 -----+ 610
 atcaagatct

Figure 19

NcoI NheI

CcATGgctAGCCCAGAAaGAaGaCCGGCCGAtATtaGaCGTGctACaGAaGctGAtATGC
 -----+-----+-----+-----+-----+-----+-----+
 ggTACcgaTCGGGTCTTtCTtCtGGCCGGCTaTAatCtGCACGaTGtCTtCGaCTaTACG
 M A S P E R R P A D I R R A T E A D M P

 CaGCaGtTtGTaCaATtGTtAAtCATtAtATaGAaACAAGtACcGTaAACTTtCgaActG
 -----+-----+-----+-----+-----+-----+-----+
 GtCGtCAaACaTGtTAaCAaTTaGTaATaTAtCTtTGTTCaTGgCATtTGAAagCtTGaC
 A V C T I V N H Y I E T S T V N F R T E

 AaCCtCAaGAACCTCAaGAaTGGACTGAtGAttTaGTCCGTtTaCGaGAGCGCTATCCtT
 -----+-----+-----+-----+-----+-----+-----+
 TtGGaGtTCTTGGaGtTCTtACCTGaCTaCTaaAtCAGGCAaAtGctCTCGCGATAGGaA
 P Q E P Q E W T D D L V R L R E R Y P W

 GGCTtGTaGCaGAaGtTgACGGaGAaGTaGCTGGgATtGCaTAtGCGGGCCCgTGGAAaG
 -----+-----+-----+-----+-----+-----+-----+
 CCGAaCaTcGtCTtCAaCTGCCTCTtCATCGaCCtTaaCGtATaCGCCCCGGGcACCTTtC
 L V A E V D G E V A G I A Y A G P W K A

 CACGaAAtGCaTATGAtTGGACgGCTGAaTCAActGTgTACGTtTCaCCaCGtCATCAaC
 -----+-----+-----+-----+-----+-----+-----+
 GTgCtTTaCGtATaCTaACCTGcCGaCTtAGtTGaCAcATGCAaAGtGGtGCaGTaGTtG
 R N A Y D W T A E S T V Y V S P R H Q R

 GgACaGGACTtGGtTCTaCtTtTaTAtACcCATCTaCTGAAaTcTtTGGAGGCACAgGGtT
 -----+-----+-----+-----+-----+-----+-----+
 CcTGtCCTGAaCCaGAaTGaaAtATaTGgGTaGAtGACTTtAGaaACCTCCGTGTcCCaA
 T G L G S T L Y T H L L K S L E A Q G F

 TtAAGAGtGTgGTaGCTGTtATaGGatTGCCgAAtGAtCCctcgGTaCGCATGCACGAaG
 -----+-----+-----+-----+-----+-----+-----+
 AaTTCTCaCAcCATCGACAaTAtCCTaACGGcTTaCTaGGgagcCATGCGTACGTgCTtC
 K S V V A V I G L P N D P S V R M H E A

 CtCTcGGATATGCTCCcaGaGGtATGtTGaGGGcCGCaGGtTTCAAaCATGGaAAtTGGC
 -----+-----+-----+-----+-----+-----+-----+
 GaGAgCCTATACGaGGgtCtCCaTACaActCCCGgCGtCCaAAGTTtGTaCCtTTaACCG
 L G Y A P R G M L R A A G F K H G N W H

 ATGAtGTaGGTTTtTGGCAaCTtGAcTTcTcttTaCCaGTACCTCCtCGTCCcGTtTtTaC
 -----+-----+-----+-----+-----+-----+-----+
 TACTaCatCCAAAaACCGTtGAaCTgAAGagaaAtGGtCATGGaGGaGCAGGgCAaaAtG
 D V G F W Q L D F S L P V P P R P V L P

BglIII

XbaI

CcGTtACtGAGATCTGATGAtctaga

GgCAaTGaCTCTAGACTACTagatct

V T E I * *

Figure 20A

NcoI NheI

ccATGgctAGCCCAGAAaGaaGaCCGGCCGAtATtaGaCGTGctACaGAaGctGAtATGC
 -----+-----+-----+-----+-----+-----+-----+-----+
 ggTACcgaTCGGGTCTTtCTtCtGGCCGGCTaTAatCtGCACGaTGtCTtCGaCTaTACG
 M A S P E R R P A D I R R A T E A D M P

CaGCaGtTtGTtACaAftGTtAatCATtATaTAaGAaACAAGtACaGTaAAtTTtcGaACTG
 -----+-----+-----+-----+-----+-----+-----+-----+
 GtCGtCAaACaTGtTAaCAaTTaGTaATaTAtCTtTGTTCaTGtCATtTAaAagCtTGaC
 A V C T I V N H Y I E T S T V N F R T E

AaCCtCAaGAACCTCAaGAaTGGACTGAtGAttTaGTaCGTtTaCGaGAaCGtTATCCTt
 -----+-----+-----+-----+-----+-----+-----+-----+
 TtGGAgtTCTTGGaGtTCTtACCTGaCTaCTaaAtCATGCAaAtGCTCTtGCaATAGGAa
 P Q E P Q E W T D D L V R L R E R Y P W

GGCTtGTaGCaGAaGtTtGACGGaGAaGTaGCTGGaATtGCaTATGCTGGtCCgTGGAAaG
 -----+-----+-----+-----+-----+-----+-----+-----+
 CCGAaCATCGtCTtCAaCTgCCTCTtCATCGaCCTTAaCGtATaCGaCCaGGcACCTTtC
 L V A E V D G E V A G I A Y A G P W K A

CacGaAAtGCaTATGAtTGGACaGCTGAaTCaACTGTtTATGTtTCaCCaCGtCATCAaC
 -----+-----+-----+-----+-----+-----+-----+-----+
 GTgCtTTaCGtATaCTaACCTGtCGaCTtAGtTGaCAaATaCAaAGtGGtGCaGTaGTtG
 R N A Y D W T A E S T V Y V S P R H Q R

GtACaGGACTtGGtTCTtACTtTaTATaCTtCATtCTtCTtAAaTCTtTGGAAgCACAAgGtT
 -----+-----+-----+-----+-----+-----+-----+-----+
 CaTGtCCTGAaCCaGAaTGaaAtATaTGaGTaGAaGAaTTtAGaaACCTtCGTGTtCCaA
 T G L G S T L Y T H L L K S L E A Q G F

TtAAaAGtGTaGTaGCTGTtATaGGatTGCCgAAaGAtCCctcaGTaCGCATGCAtGAaG
 -----+-----+-----+-----+-----+-----+-----+-----+
 AaTTtTCaCATCATCGACAaTATCCTaACGGcTTaCTaGGgagtCATGCGTACGTaCTtC
 K S V V A V I G L P N D P S V R M H E A

CtCTtGGATATGCTCCcaGaGGtATGtTGaGGGCaGCaGGtTTCAaACatGGaAAtTGGC
 -----+-----+-----+-----+-----+-----+-----+-----+
 GaGAaCCTIATACGaGGgtCtCCaTACaACTCCCgTCCgTCCaAAGTTtGTaCCTTTaACCG
 L G Y A P R G M L R A A G F K H G N W H

ATGAtGTaGGTTTtTGGCAaCTtGAaCTTCTtcttTaCCaGTACCTCCTCGTCCcGTtTtAc
 -----+-----+-----+-----+-----+-----+-----+-----+
 TACTaCATCCAAAaACCGTtGAaCTgAAGagaaAtGGtCATGGaGGaGCAGGgCAaaAtG
 D V G F W Q L D F S L P V P P R P V L P

BglII

XbaI

CcGTtActGAGATCTGATGAtctaqa

GgCAaTGaCTCTAGACTACTagatct

V T E I * *

Figure 20B

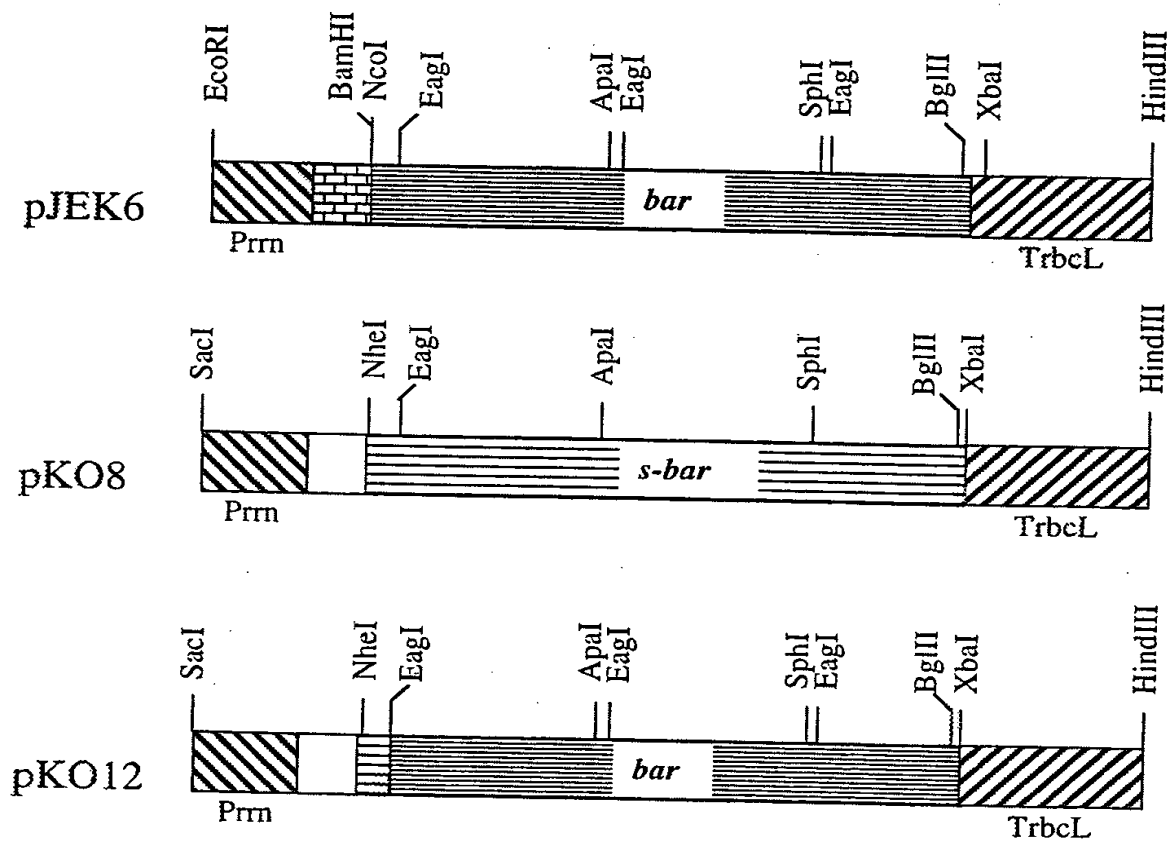


Figure 21

Bacterial Extracts

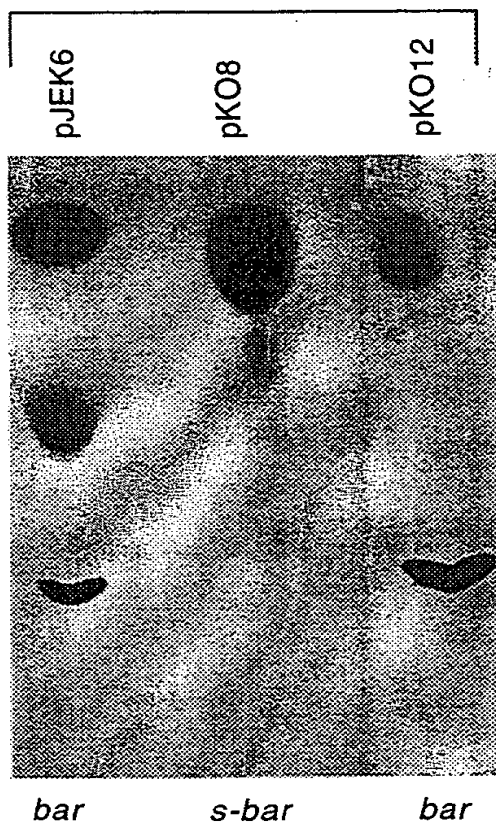


Figure 22A

Plant Extracts

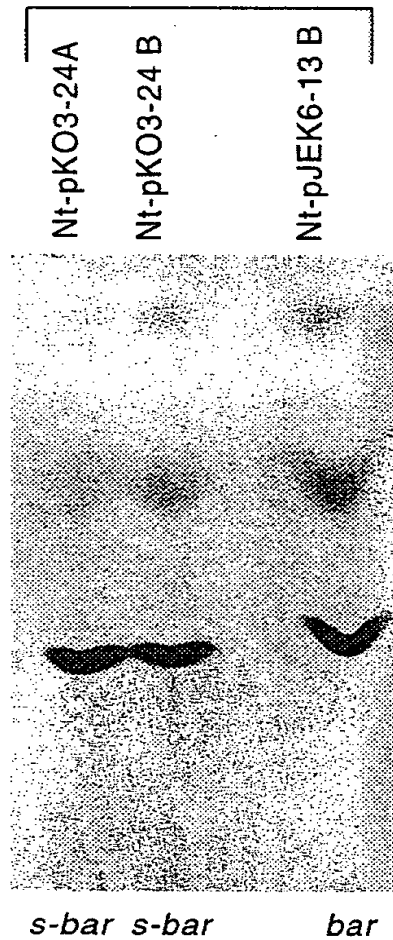


Figure 22B

AAD E L V E G K L E L V E G L K V A GFP
 GGTAAGTGGCAAAgaactgttgaaaggaaattggagctagtagaaggctcttaaagtcgCCATGG
 BstXI NcoI

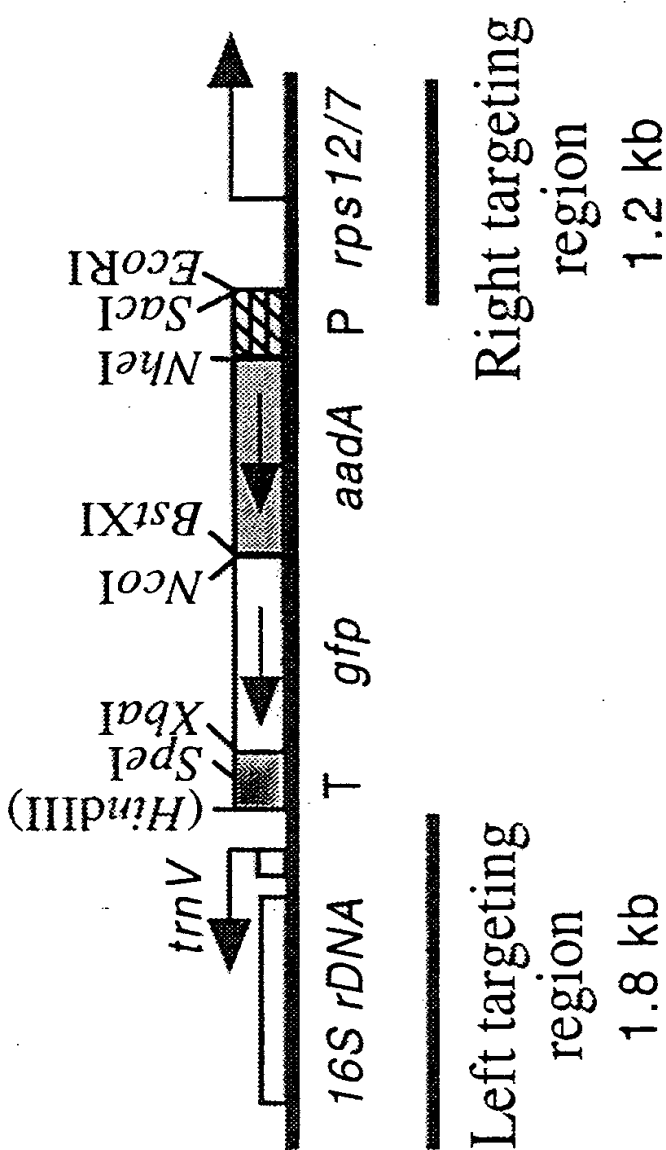


Figure 23A

Figure 23B

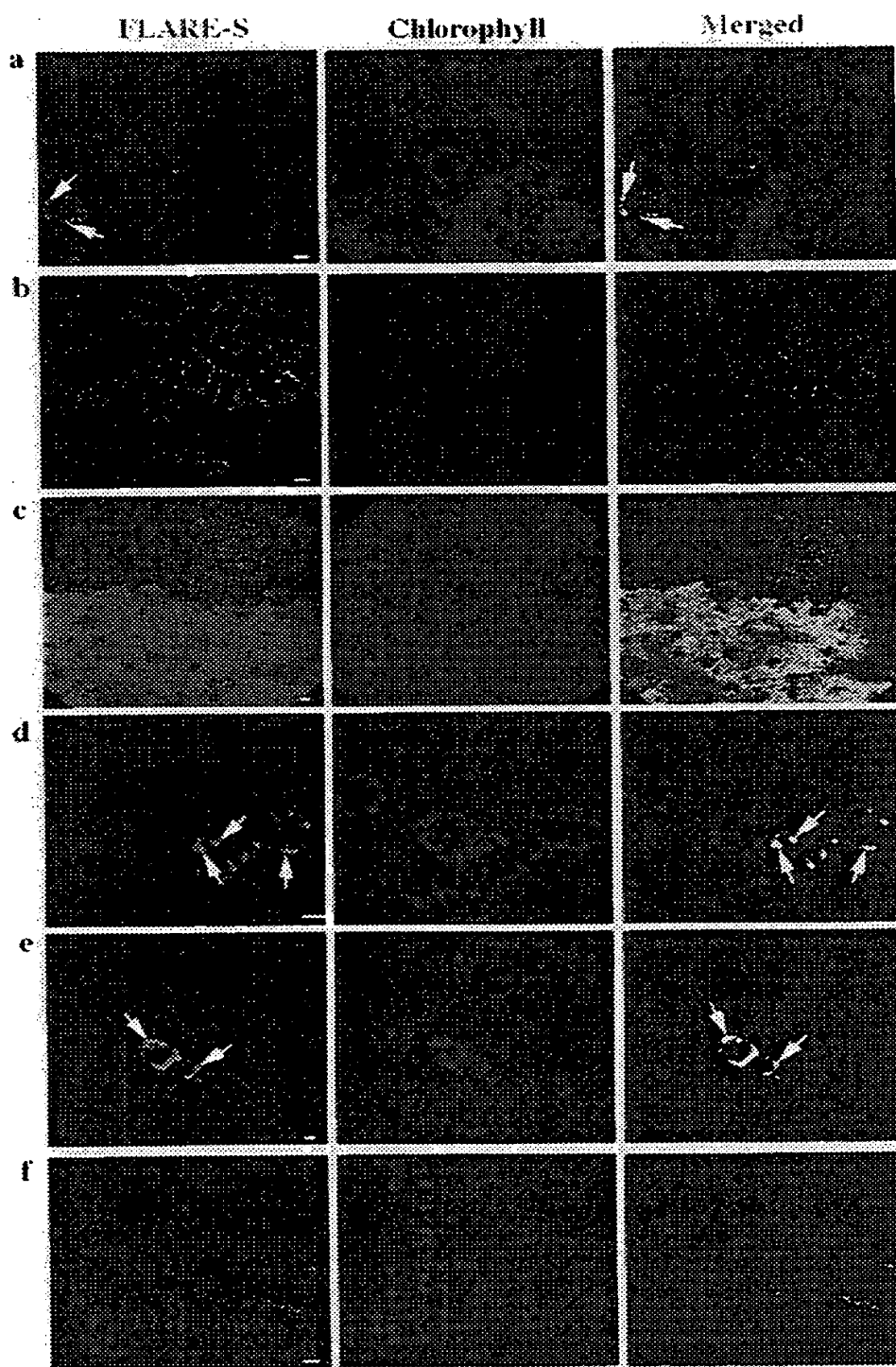
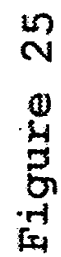


Figure 24



38/49

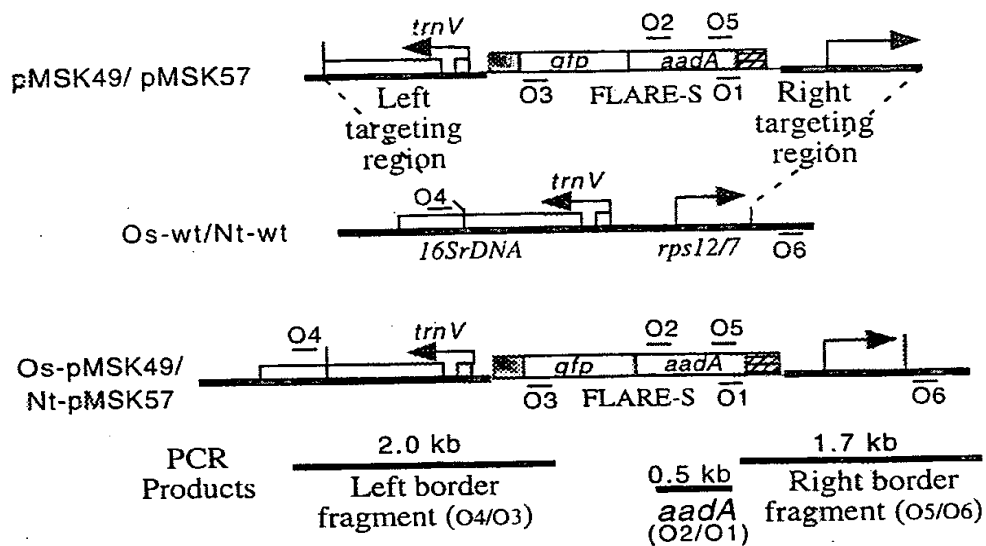


Figure 26A

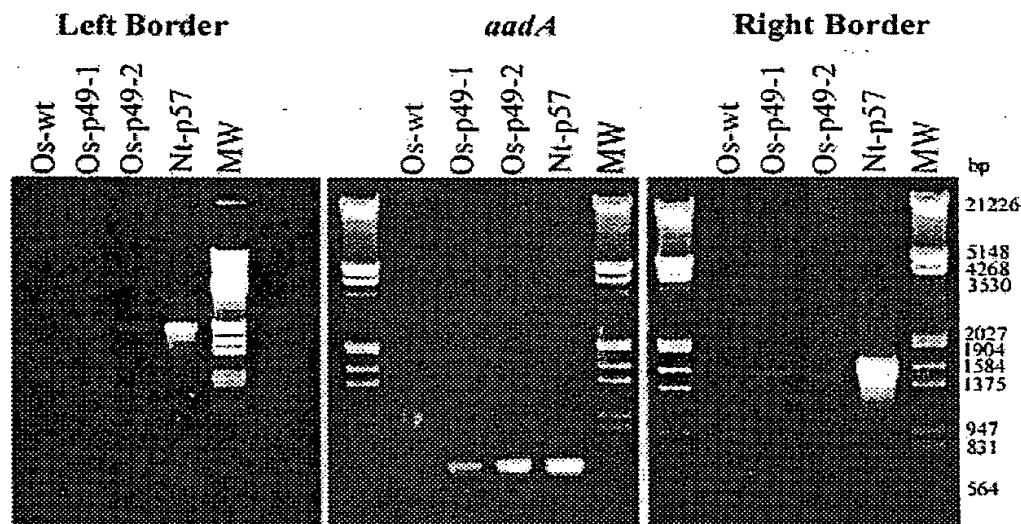


Figure 26B

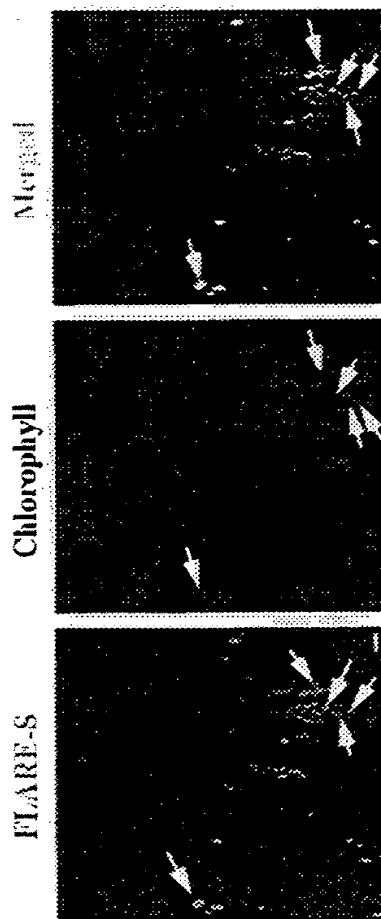


Figure 27

FLARE16-S.seq Length: 1574

1 ccATGgGGgc tagcGAAGCG GTGATCGCCG AAGTATCGAC TCAACTATCA
 51 GAGGTAGTTG GCGTCATCGA GCGCCATCTC GAACCGACGT TGCTGGCCGT
 101 ACATTTGTAC GGCTCCGCGG TGGATGGCGG CCTGAAGCCA CACAGTGATA
 151 TTGATTGCT GGTACGGTG ACCGTAAAGTC TTGATGAAAC AACGCGGCCGA
 201 GCTTTGATCA ACGACCTTTT GGAAACTTCG GCTTCCCCTG GAGAGAGCGA
 251 GATTC¹CCGC GCTGTAGAAG TCACCATTGT TGTGCACGAC GACATCATTC
 301 CGTGGCGTTA TCCAGCTAAG CGCGAACTGC AATTTGGAGA ATGGCAGCGC
 351 AATGACATTC TTGCAGGTAT CTTGAGCCCA GCCACGATCG ACATTGATCT
 401 GGCTATCTTG CTGACAAAAG CAAGAGAACA TAGCGTTGCC TTGGTAGGTC
 451 CAGCGGCGGA GGAACCTTTT GATCCGGTTC CTGAACAGGA TCTATTTGAG
 501 GCGCTAAATG AAACCTTAAC GCTATGGAAC TCGCCGCCCCG ACTGGGCTGG
 551 CGATGAGCGA AATGTAGTGC TTACGTTGTC CCGCATTGGG TACAGCGCAG
 601 TAACCGGCAA AATCGCGCCG AAGGATGTCT CTGCCGACTG GGCAATGGAG
 651 CGCCTGCCGG CCCAGTATCA GCCCGTCATA CTTGAAGCTA GACAGGCTTA
 701 TCTTGACAA GAAGAAGATC GCTTGGCCTC GCGCGCAGAT CAGTTGGAAG
 751 AATTTGTCCA CTACGTGAAA GGCAGATCA CCAAGGTAGT gggcaaagaa
 801 cttgttgaag gaaaattgga gctagtagaa ggtcttaaag tgcgc¹ATGgc
 851 CAGTAAAGGA GAAGA¹CTTT TCACTGGAGT TGTCCCAATT CTTGTTGAAT
 901 TAGATGGTGA TGTTAATGGG CACAAATTTT CTGTCAGTGG AGAGGGTGAA
 951 GGTGATGCAA CATACGGAAA ACTTACCCCT AAATTTATTT GCACTACTGG
 1001 AAAACTACCT GTTCCTTGGC CAACACTTGT CACTACTTTC TCTTATGGTG
 1051 TTCAATGCTT TTCAAGATAC CCAGATCATA TGAAGCGGCA CGACTTCTTC
 1101 AAGAGCGCCA TGCCTGAGGG ATACGTGCAG GAGAGGACCA TCTCTTTCAA
 1151 GGACGACGGG AACTACAAGA CACGTGCTGA AGTCAAGTTT GAGGGAGACA
 1201 CCTCGTCAA CAGGATCGAG CTTAAGGGAA TCGATTTCAA GGAGGACGGA
 1251 AACATCCTCG GCCACAAGTT GGAATACAAC TACAAC¹CCC ACAACGTATA
 1301 CATCACGGCA GACAAACAAA AGAATGGAAT CAAAGCTAAC TTCAA¹AATTA
 1351 GACACAACAT TGAAGATGGA AGCGTTCAAC TAGCAGACCA TTATCAACAA
 1401 AATACTCCAA TTGGCGATGG CCCTGTCCCT TTACCAGACA ACCATTACCT
 1451 GTCCACACAA TCTGCCCTTT CGAAAGATCC CAACGAAAAG AGAGACCACA
 1501 TGGTCCTTCT TGAGTTTGA ACAGCTGCTG GGATTACACA TGGCATGGAT
 1551 GAACTATACA AATAAG¹ctc taga

XbaI

Figure 28

FLARE16-S1.seq Length: 1953

1 **SacI**
 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
 101 CTTGTTGTTG TGAA AATTCT TAATTCATGA GTTGTAGGGA GGGATTTATG
 151 TCACCACAAA CAGAGACTAA AGCAAGTGTG GGATTCAAA ctagcGAAGC
 201 GGTGATCGCC GAAGTATCGA CTCAACTATC AGAGGTAGTT GGCCTCATCG
 251 AGCGCCATCT CGAACCGACG TTGCTGGCCG TACATTTGTA CGGCTCCGCA
 301 GTGGATGGCG GCTGAAGCC ACACAGTGAT ATTGATTGTC TGGTTACGGT
 351 GACCGTAAGG CTTGATGAAA CAACGCGGCG AGCTTTGATC AACGACCTTT
 401 TGGAAACTTC GGCTTCCCCT GGAGAGAGCG AGATTCTCCG CGCTGTAGAA
 451 GTCACCATTG TTGTGCACGA CGACATCATT CCGTGGCGTT ATCCAGCTAA
 501 GCGCGAACTG CAATTTGGAG AATGGCAGCG CAATGACATT CTTGCAGGTA
 551 TCTTCGAGCC AGCCACGATC GACATTGATC TGGCTATCTT GCTGACAAAA
 601 GCAAGAGAAC ATAGCGTTGC CTTGGTAGGT CCAGCGGCGG AGGAACTCTT
 651 TGATCCGGTT CCTGAACAGG ATCTATTTGA GCGCTAAAT GAAACCTTAA
 701 CGCTATGGAA CTCGCCGCC GACTGGGCTG GCGATGAGCG AAATGTAGTG
 751 CTTACGTTGT CCCGCATTG GTACAGCGCA GTAACCGGCA AAATCGCGCC
 801 GAAGGATGTC GCTGCCGACT GGGCAATGGA GCGCCTGCCG GCCCAGTATC
 851 AGCCCGTCAT ACTTGAAGCT AGACAGGCTT ATCTTGGACA AGAAGAAGAT
 901 CGCTTGGCCT CGCGCGCAGA TCAGTTGGAA GAATTGTGCC ACTACGTGAA
 951 AGGCGAGATC ACCAAGGTAG TGGGCAAAga acttggtgaa ggaacattg
 1001 agctagtaga aggtcttaaa gtcgccaTgG CTAGTAAAGG AGAAGAAGCTT
 1051 TTCCTGGAG TTGTCCCAAT TCTTGTGAA TTAGATGGTG ATGTTAATGG
 1101 GCACAAATTT TCTGTCAGTG GAGAGGGTGA AGGTGATGCA ACATACGGAA
 1151 AACTTACCCT TAAATTTATT TGCACTACTG GAAACTACC TGTTCTTGG
 1201 CCAACACTTG TCACTACTTT CTCTTATGGT GTTCAATGCT TTTCAAGATA
 1251 CCCAGATCAT ATGAAGCGGC ACGACTTCTT CAAGAGCGCC ATGCCTGAGG
 1301 GATACGTGCA GGAGAGGACC ATCTCTTTCA AGGACGACGG GAACTACAAG
 1351 ACACGTGCTG AAGTCAAGTT TGAGGGAGAC ACCCTCGTCA ACAGGATCGA
 1401 GCTTAAGGGA ATCGATTTC AAGGAGACGG AAACATCCTC GGCCACAAGT
 1451 TGGAATACAA CTACAATCC CACAACGTAT ACATCACGGC AGACAAACAA
 1501 AAGAATGGAA TCAAAGCTAA CTTCAAAATT AGACACAACA TTGAAGATGG
 1551 AAGCGTTCAA CTAGCAGACC ATTATCAACA AAATACTCCA ATTGGCGATG
 1601 GCCCTGTCTT TTTACCAGAC AACCATTACC TGTCCACACA ATCTGCCCTT
 1651 TCGAAAGATC CCAACGAAA GAGAGACCAC ATGGTCCTTC TTGAGTTTGT
 1701 AACAGCTGCT GGGATTACAC ATGGCATGGA TGAACATAC AAATAAGgct
 1751 ctagagcCAT CCTGGCCTAG TCTATAGGAG GTTTTGAAAA GAAAGGAGCA
 1801 ATAATCATTT TCTTGTCTA TCAAGAGGGT GCTATTGCTC CTTTCTTTT
 1851 TTCTTTTAT TTATTTACTA GTATTTTACT TACATAGACT TTTTGTTTA
 1901 CATTATAGAA AAAGAAGGAG AGGTTATTTT CTTGCATTTA TTCATGaaag
 1951 ctt

Lap808

aadA

gfp

TpsbA

HindIII

Figure 29

09/762105

FLARE16-S2.seq Length: 1985

1 *Sact*
 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG AATTAACCGA
 101 TCGACGTGCa AGCGGACATT TATTTTaaAT TCGATAATTT TTGCAAAAAC
 151 ATTTGACAT ATTTATTTAT TTTATTATTA TGAGAATCAA TCCTACTACT
 201 TCTGGTTCG GGGTTTCCAC GgctagcGAA GCGGTGATCG CCGAAGTATC
 251 GACTCAACTA TCAGAGGTAG TTGGCGTCAT CGAGCGCCAT CTCGAACCGA
 301 CGTTGCTGGC CGTACATTTG TACGGCTCCG CAGTGGATGG CGGCCTGAAG
 351 CCACACAGTG ATATTGATTT GCTGGTTACG GTGACCGTAA GGCTTGATGA
 401 AACCAACGCG CGAGCTTTGA TCAACGACCT TTTGGAAACT TCGGCTTCCC
 451 CTGGAGAGAG CGAGATTCTC CGCGCTGTAG AAGTCACCAT TGTTGTGCAC
 501 GACGACATCA TTCCGTGGCG TTATCCAGCT AAGCGCGAAC TGCAATTTGG
 551 AGAATGGCAG CGCAATGACA TTCTTGACAG TATCTTCGAG CCAGCCACGA
 601 TCGACATTGA TCTGGCTATC TTGCTGACAA AAGCAAGAGA ACATAGCGTT
 651 GCCTTGGTAG GTCCAGCGGC GGAGGAACTC TTTGATCCGG TTCCTGAACA
 701 GGATCTATTT GAGGCGCTAA ATGAAACCTT AACGCTATGG AACTCGCCGC
 751 CCGACTGGGC TGGCGATGAG CGAAATGTAG TGCTTACGTT GTCCCGCATT
 801 TGGTACAGCG CAGTAACCGG CAAAATCGCG CCGAAGGATG TCGCTGCCGA
 851 CTGGGCAATG GAGCGCCTGC CGGCCCGTA TCAGCCCGTC ATACTTGAAG
 901 CTAGACAGGC TTATCTTGGG CAAGAAGAAG ATCGCTTGGC CTCGCGCGCA
 951 GATCAGTTGG AAGAATTTGT CCCTACGTC AAAGGCGAGA TCACCAAGGT
 1001 AGTGGCAA gaacttggtg aaggaaaatt ggaagctagta gaaggtctta
 1051 aagtcgccAT GgctAGTAAa GGAGAAGAAC TTTTCACTGG AGTTGTCCCA
 1101 ATTCTTGTG AATTAGATGG TGATGTTAAT GGGCACAAAT TTTCTGTCAG
 1151 TGGAGAGGGT GAAGGTGATG CAACATACGG AAAACTTACC CTTAAATTTA
 1201 TTTGCACTAC TGGAAACTA CCTGTTCCtT GGCCAACACT TGTCATACT
 1251 TTCTCTTATG GTGTTCAATG CTTTCAAGA TACCCAGATC ATATGAAGCG
 1301 GCACGACTTC TTCAAGAGCG CCATGCCTGA GGGATACGTG CAGGAGAGGA
 1351 CCATCTCTTT CAAGGACGAC GGGAACTACA AGACACGTGC TGAAGTCAAG
 1401 TTTGAGGGAG ACACCCCTCGT CAACAGGATC GAGCTTAAGG GAATCGATTT
 1451 CAAGGAGGAC GGAAACATCC TCGGCCACAA GTTGAATAC AACTACAAC
 1501 CCCACAACGT ATACATCAGG GCAGACAAAC AAAAGAATGG AATCAAAGCT
 1551 AACTTCAAAA TTAGACACAA CATTGAAGAT GGAAGCGTTC AACTAGCAGA
 1601 CCATTATCAA CAAAATACTC CAATTGGCGA TGGCCCTGTC CTTTACCAG
 1651 ACAACCATTA CCTGTCCACA CAATCTGCCC TTTCGAAAGA TCCCAACGAA
 1701 AAGAGAGACC ACATGGTCCT TCTTGAGTTT GTAACAGCTG CTGGGATTAC
 1751 ACATGGCATG GATGAACAT ACABAATAAGg ctctagagc ATCCTGGCCT
 1801 AGTCTATAGG AGGTTTGGAA AAGAAAGGAG CAATAATCAT TTTCTTGTTT
 1851 TATCAAGAGG GTGCTATTGC TCCTTTCTTT TTTCTTTTT ATTTATTTAC
 1901 TAGTATTTTA CTTACATAGA CTTTTTGTG TACATTATAG AAAAAGBAGG
 1951 AGAGGTTATT TTCTTGCAAT TATTCATGaa agctt
 HmaIII

Lrbd DB
oada
gfp
Tp56A

Figure 30

FLARE11-S.seq Length: 1595

1 **NcoI** **C-Myc**
 ccatgggggc tagcgaacaa aaactcattt ctgaagaaga cttgcctagc
 51 GAAGCGGTGA TCGCCGAAGT ATCGACTCAA CTATCAGAGG TAGTTGGCGT
 101 CATCGAGCGC CATCTCGAAC CGACGTTGCT GGCCGTACAT TTGTACGGCT
 151 CCGCAGTGGT TGGCGGCTG AAGCCACACA GTGATATTGA TTTGCTGGTT
 201 ACGGTGACCG TAAGGCTTGA TGAAACAACG CGGCGAGCTT TGATCAACGA
 251 CCTTTTGGAA ACTTCGGCTT CCCCTGGAGA GAGCGAGATT CTCCGCGCTG
 301 TAGAAGTCAC CATTGTTGTG CACGACGACA TCATTCCGTG GCGTTATCCA
 351 GCTAAGCGCG AACTGCAATT TGGAGAATGG CAGCGCAATG ACATTCTTGC
 401 AGGTATCTTC GAGCCAGCCA CGATCGACAT TGATCTGGCT ATCTTGCTGA
 451 CAAAAGCAAG AGAACAATAG GTTGCCTTGG TAGGTCCAGC GCGGGAGGAA
 501 CTCTTTGATC CGGTTCTCTA ACAGACTCTA TTTGAGGCGC TAAATGAAAC
 551 CTTAACGCTA TGGAACTCGC GCCTCGACTG GGCTGGCGAT GAGCGAAATG
 601 TAGTGCTTAC GTTGTCCTGC ATTTGGTACA GCGCAGTAAC CGGCAAATC
 651 GCGCCGAAGG ATGTCGCTGC CGACTGGGCA ATGGAGCGCC TGCCGGCCCA
 701 GTATCAGCCC GTCATACTTG AAGCTAGACA GGCTTATCTT GGACAAGAAG
 751 AAGATCGCTT GGCCTCGCGC GCAGATCAGT TGGAGAAGATT TGTCCACTAC
 801 GTGAAGGCG AGATCACCAA GGTAGTGGC AAAGaaacttg cagttgaagg
 851 aaaattggag gtccgcatg ctagtaaagg AGAAGAACTT TTCACTGGAG
 901 TTGTCCCAAT TCTTGTTGAA TTAGATGGTG ATGTTAATGG GCACAAATTT
 951 TCTGTCAGTG GAGAGGGTGA AGGTGATGCA ACATACGGAA AACTTACCCT
 1001 TAAATTTATT TGCATACTG GAAACTACC GTTCCCTGG CCAACACTTG
 1051 TCACTACTTT CTCTTATGGT GTTCAATGCT TTTCAAGATA CCCAGATCAT
 1101 ATGAAGCGGC ACGACTTCTT CAAGAGCGCC ATGCCTGAGG GATACGTGCA
 1151 GGAGAGGACC ATCTCTTTCA AGGACGACGG GAACTACAAG ACACGTGCTG
 1201 AAGTCAAGTT TGAGGGAGAC ACCCTCGTCA ACAGGATCGA GCTTAAGGGA
 1251 ATCGATTTC AAGGAGACGG AAACATCCTC GGCCACAAGT TGGAAATACAA
 1301 CTACAACTCC CACAACGIAT ACATCAGGGC AGACAAACAA AAGAATGGAA
 1351 TCAAAGCTAA CTTCAAAATT AGACACAACA TTGAAGATGG AAGCGTTCAA
 1401 CTAGCAGACC ATTATCAACA AAATACTCCA ATTGGCGATG GCCCTGTCCT
 1451 TTTACCAGAC AACCATTACC TGTCCACACA ATCTGCCCTT TCGAAAGATC
 1501 CCAACGAAAA GAGAGACCAC ATGGTCCTTC TTGAGTTGT AACAGCTGCT
 1551 GGGATTACAC ATGGCATGGA TGAAGTATAC AAATAAGgct ctaga

XbaI

Figure 31

FLARE11-S3.seq Length: 1961

1 SacI
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG GGAGACCACA
 101 ACGGTTTCCC aCTAGAAATA ATTTTGTTTA ACTTTAAGAA GGAGATATAC
 151 ATATGGCaAG CATGACTGGT GGACAGgcta gcgaacaaaa actcatttct
 201 gaagaagact tgcctagcGA AGCGGTGATC GCCGAAGTAT CGACTCAACT
 251 ATCAGAGGTA GTTGGCGTCA TCGAGCGCCA TCTCGAACCG ACGTTGCTGG
 301 CCGTACATTT GTACGGCTCC GCAGTGGATG GCGGCCTGAA GCCACACAGT
 351 GATATTGATT TGCTGGTTAC GGTGACCGTA AGGCTTGATG AAACAACGCG
 401 GCGAGCTTTG ATCAACGACC TTTTGGAAAC TTCGCTTCC CCTGGAGAGA
 451 GCGAGATTCT CCGCGCTGTA GAAGTCACCA TTGTTGTGCA CGACGACATC
 501 ATTCCGTGGC GTTATCCAGC TAAGCGCGAA CTGCAATTTG GAGAATGGCA
 551 GCGCAATGAC ATTCTTGCA GATCTTCGA GCCAGCCACG ATCGACATTG
 601 ATCTGGCTAT CTTGCTGACA AAAGCAAGAG AACATAGCGT TGCCTTGGTA
 651 GGTCCAGCGG CCGAGGAACT CTTTGATCCG GTTCCTGAAC AGGATCTATT
 701 TGAGGCGCTA AATGAAACCT TAACGCTATG GAACTCGCCG CCCGACTGGG
 751 CTGGCGATGA GCGAAATGTA GTGCTTACGT TGTCCCGCAT TTGGTACAGC
 801 GCAGTAACCG GCAAAATCGC GCCGAAGGAT GTCGCTGCCG ACTGGGCAAT
 851 GGAGCGCCTG CCGGCCAGT ATCAGCCCGT CATACTTGAA GCTAGACAGG
 901 CTTATCTTGG ACAAGAAGAA GATCGCTTGG CCTCGCGCGC AGATCAGTTG
 951 GAAGAATTTG TCCACTACGT GAAAGGCGAG ATCACCAGG TAGTgGGCAA
 1001 ggaacttgca gttgaaggaa aattggaggt cgccATGgct AGTAAAGGAG
 1051 AAGAACTTTT CACTGGAGTT GTCCCAATTC TTGTTGAATT AGATGGTGAT
 1101 GTTAATGGGC ACAAAATTTT TGTCAGTGA GAGGGTGAAG GTGATGCAAC
 1151 ATACGGAAAA CTTACCCTTA AATTTATTTG CACTACTGGA AAACCTACCTG
 1201 TTCctTGGCC AACACTTGTC ACTACTTTCT CTTATGGTGT TCAATGCTTT
 1251 TCAAGATACC CAGATCATAT GAAGCGGCAC GACTTCTTCA AGAGCGCCAT
 1301 GCCTGAGGGA TACGTGCAGG AGAGGACCAT CTCTTTCAAG GACGACGGGA
 1351 ACTACAAGAC ACGTGCTGAA GTCAAGTTTG AGGGAGACAC CCTCGTCAAC
 1401 AGGATCGAGC TTAAGGGAAT CGATTTCAG GAGGACGGAA ACATCCTCGG
 1451 CCACAAGTTG GAATACAACCT ACAACTCCCA CAACGTATAC ATCACGGCAG
 1501 ACAACAACAA GAATGGAATC AAAGCTAACT TCAAAATTAG ACACAACATT
 1551 GAAGATGGAA GCGTTCAACT AGCAGACCAT TATCAACAAA ATACTCCAAT
 1601 TGGCGATGGC CCTGTCCTTT TACCAGACAA CCATTACCTG TCCACACAAT
 1651 CTGCCCTTTC GAAAGATCCC AACGAAAAGA GAGACCACAT GGTCCTTCTT
 1701 GAGTTTGTA CAGCTGCTGG GATTACACAT GGCATGGATG AACTATACAA
 1751 ATAAGgctct agagcTATCC TGGCCTAGTC TATAGGAGGT TTTGAAAAGA
 1801 AAGGAGCAAT AATCATTTTC TTGTTCTATC AAGAGGGTGC TATTGCTCCT
 1851 TTCTTTTTTT CTTTTATTT ATTTACTAGT ATTTTACTTA CATAGACTTT
 1901 TTTGTTTACA TTATAGAAAA AGAAGGAGAG GTTATTTTCT TGCATTTATT
 1951 CATGaaagct t

HindIII

LT781008

aadA

gfp

TpsA

Figure 32

pMSK35.seq Length: 4671

Figure 33A

122488

1	GGGAACGGAT	TCACCGCCGT	ATGGCTGACC	GGCGATTACT	AGCGATTCTT
51	GCTTCATGCA	GGCGAGTTGC	AGCCTGCAAT	CCGAACTGAG	GACGGGTTTT
101	TGGAGTTAGC	TCACCCTCGC	GAGATCGCGA	CCCTTTGTCC	CGCCCATTGT
151	AGCACGTGTG	TCGCCCAGGG	CATAAGGGGC	ATGATGACTT	GGCCTCATCC
201	TCTCCTTCCT	CCGGCTTAAC	ACCGGCGGTC	TGTTCAGGGT	TCCAAACTCA
251	TAGTGGCAAC	TAAACACGAG	GGTTGCGCTC	GTTGCGAGAC	TTAACCCAAC
301	ACCTTACGGC	ACGAGCTGAC	GACAGCCATG	CACCACCTGT	GTCCGCGTTC
351	CCGAGGGCAC	CCCTCTCTTT	CAAGAGGATT	CGCGGCATGT	CAAGCCCTGG
401	TAAGGTTCTT	CGCTTTGCAT	CGAATTAAAC	CACATGCTCC	ACCGCTTGTG
451	CGGGCCCCCG	TCAATTCCTT	TGAGTTTCAT	TCTTGCGAAC	GTACTCCCCA
501	GGCGGGATAC	TTAACGCGTT	AGCTACAGCA	CTGCACGGGT	CGAGTCGCAC
551	AGCACCTAGT	ATCCATCGTT	TACGGCTAGG	ACTACTGGGG	TCTCTAATCC
601	CATTTGCTCC	CCTAGCTTTC	GTCTCTCAGT	GTCAGTGTCC	GCCCAGCAGA
651	GTGCTTTTCG	CGTTGGTGT	CTTTCCGATC	TCAATGCATT	TCACCGCTCC
701	ACCGGAAATT	CCCTCTGCCC	CTACCGTACT	CCAGCTTGGT	AGTTTCCACC
751	GCCTGTCCAG	GGTTGAGCCC	TGGGATTGTA	CGGCGGACTT	GAAAAGCCAC
801	CTACAGACGC	TTTACGCCCA	ATCATTCCGG	ATAACGCTTG	CATCCTCTGT
851	CTTACCGCGG	CTGCTGGCAC	AGAGTTAGCC	GATGCTTATT	CCTCAGATAC
901	CGTCATTGTT	TCTTCTCGA	GAAAAGAAGT	TGACGACCCG	TGGGCCTTCC
951	ACCTCCACGC	GGCATTGCTC	CGTCAGGCTT	TCGCCCATTG	CGGAAAATTC
1001	CCCACIGCTG	CCTCCCGTAG	GAGTCTGGGC	CGTGTCTCAG	TCCCAGTGTG
1051	GCTGATCATC	CTCTCGGACC	AGCTACTGAT	CATCGCCTTG	GTAAGCTATT
1101	GCCTCACCAA	CTAGCTAATC	AGACGCGAGC	CCCTCCTTGG	GCGGATTTCT
1151	CCTTTTGTCT	CTCAGCCTAC	GGGGTATTAG	CAACCGTTTC	CAGTTGTTGT
1201	TCCCTTCCCA	AGGGCAGGTT	CTTACGCGTT	ACTCACCCGT	TCGCCACTGG
1251	AAACACCACT	TCCCGTTCEA	CTTGCAATGT	TTAAGCATGC	CGCCAGCGTT
1301	CATCCTGAGC	CAGGATCGAA	CTCTCCATGA	GATTCAAGT	TGCATTACTT
1351	ATAGCTTCCT	TATTTCGTAG	CAAAGCGGAT	TCCGAATTGT	CTTTCCTTCC
1401	AAGGATAACT	TGTATCCATG	CGCTTCAGAT	TATTAGCCTG	GAGTTCGCCA
1451	CCAGCAGTAT	AGCCAACCTT	ACCCTATCAC	GTCAATCCCA	CAAGCCTCTT
1501	ATCCATTCCC	GTTTCGATCGT	GGCGGGGGGA	GTAAGTCAA	ATAGAAAAAA
1551	CTCACATTGG	GTTTAGGGAT	AATCAGGCTC	GAACTGATGA	CTTCCACCAC
1601	GTCAGAGTGA	CACCTACCCG	CTGAGTTATA	TCCCTTCCEC	GTCCCTCGA
1651	GAAAGGAAT	TACCGAATCC	TAGGCCAAAG	GGGCGAGAAA	CTCAAGGCCA
1701	CCCTTCTTCC	GGGCTTTCTT	TCCACACTAT	TATGGATAGT	CAAATAATGG
1751	GAAAAATTGG	ATTCAATTGT	CAACCGGTCC	TATCGAAAAT	AGGATTGACT
1801	ATGGATTCTG	GCCATAGCAC	ATGGTTTCAT	AAAACTGTGA	CGATTTTCCC
1851	GATCTAATC	GAGCAGGTTT	CCATGAAGAA	gatcgacggt	atcgataagc
1901	ttgcatgcct	gcaggtCGAA	TATAGCTCTT	CTTCTTATT	TCAATGATAT
1951	TATTATTTCA	AAGATAAGAG	ATATTCAAAG	ATAAGAGATA	AGAAGAAGTC
2001	AAAATTTGAT	TTTTTTTTTG	GAAAAAATA	ATCAAAAAGA	TATAGTAACA
2051	TTAGCAAGAA	GAGAAACAAG	TTCTATTCCA	CAATTTAAAC	AAATACAAAA
2101	TCAAAATAGA	ATACTCAATC	ATGAATAAAT	GCAAGAAAAT	AACCTCTCCT
2151	TCTTTTCTA	TAATGTAAAC	AAAAAAGTCT	ATGTAAGTAA	AATACTAGTA
2201	AATAAATAAA	AAGAAAAATA	GAAAGGAGCA	ATAGCACCTT	CTTGATAGAA
2251	CAAGAAAATG	ATTATTGCTC	CTTCTTTTTC	AAAACCTCCT	ATAGACTAGG
2301	CCAGGATCgc	tctagcTAGA	CATTATTGTC	CGACTACCTT	GGTGATCTCG
2351	CCTTTCACGT	AGTGGACAAA	TTCTTCCAAC	TGATCTGCGC	GCGAGGCCAA
2401	GCGATCTTCT	TCTTGTTCAA	GATAAGCCTG	TCTAGCTTCA	AGTATGACGG
2451	GCTGATACTG	GGCCGGCAGG	CGCTCCATTG	CCCAGTCGGC	AGCGACATCC
2501	TTCCGGCGCG	TTTGCCGGT	TACTGCGCTG	TACCAAATGC	GGGACAACGT
2551	AAGCACTACA	TTTCGTCAT	CGCCAGCCCA	GTCGGGCGGC	GAGTTCCATA
2601	GCGTTAAGGT	TTCATTAGC	GCCTCAAATA	GATCCTGTTC	AGGAACCGGA
2651	TCAAAGAGTT	CCTCCGCCGC	TGGACCTACC	AAGGCAACGC	TATGTTCTCT
2701	TGCTTTTGTG	AGCAAGATAG	CCAGATCAAT	GTCGATCGTG	GCTGGCTCGA

Rice left targeting sequence

acida

pMSK35.seq Length: 4671

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2751 AGATACCTGC AAGAATGTCA TTGCGCTGCC ATTCTCCAAA TTGCAGTTCG
2801 CGCTTAGCTG GATAACGCCA CGGAATGATG TCGTCGTGCA CAACAATGGT
2851 GACTTCTACA GCGCGGAGAA TCTCGCTCTC TCCAGGGGAA GCCGAAGTTT
2901 CCAAAAGGTC GTTGATCAAA GCTCGCCGCG TTGTTTCATC AAGCCTTACG
2951 GTCACCGTAA CCAGCAAATC AATATCACTG TGTGGCTTCA GGCCGCCATC
3001 CACTGCGGAG CCGTACAAAT GTACGGCCAG CAACGTCGGT TCGAGATGGC
3051 GCTCGATGAC GCCAACTACC TCTGATAGTT GAGTCGATAC TTCGGCGATC
3101 ACCGCTTCCC TCATGgATCC CTCCTACAA CTGTATCCa GCGCTTCgTA
3151 TTCGCCCGGA GTTCGCTCCC AGAAATATAG CCATCCCTGC CCCCTCACGT
3201 CAATCCCACG AGCCTCTTAT CCATTCTCAT TGAACGACGG CGGGGGAGC
3251 ttgggtaccg agctcgaatt cctgcagccc gatcTTACCA TTTCCGAAGG
3301 AACTGGGGCT ACATTTCTTT TCAATTTCCA TTCAAGAGTT TCTTATCTGT
3351 TTCCACGCCC TTTTTTGAGA CCTCGAAACA TGAAATGGAC AAATTCCTTC
3401 TCTTAGGAAC ACATACAAGA AAAAGGATAA TGGTAGCCCT CCCATTAAC
3451 ACTTCATTTT ATTTATGAAT TTCATAGTAA TAGAAATCCA TGTCTACCG
3501 AGACAGAATT TCGAACTTGC TATCCTCTTG CCTAATAGGC AAAGATTGAC
3551 CTCTGTAGAA AGAATGATTC ATTCGGATCG ATATGAGGAC CCAACTACGT
3601 TGCATTGCAG AATCCATGTT CCATATTTGA AGAGGGTTGA CCTCTGTGCT
3651 TCTCTCATGG TACAATCCTC TTCCTGCTGA GCCCCCTTC TCCTCGGTCC
3701 ACAGAGAAAA AATGGAGGAC TGGTGCUGAC AGTTCATCAC GGAAGAAAGA
3751 ACTCACAGAG CCGGGATCGC TAACTAATAG AATAGTACTA CTAATAATA
3801 CTAATATATA GAAATAGATA Tctagctaga AATAGAAACA ACTAATATAT
3851 AGATAATCGA AATTGAAAAG AACTGTCTTT TCTGTATACT TTCCCCGTTT
3901 TATTGCTACC GCGGGTCTTA TGCAATCGAT CGGATCATAT AGATATCCCT
3951 TCAACACAAC ATAGGTCATC GAAAGGATCT CGGACGACTC ACCAAAGCAC
4001 GAAAGCCAGT TAGAAAATGG ATTCCTATTT GAAGAGTGCC TAACCGCATG
4051 GATAAGCTCA CATTAAACCG TCAATTTTGG ATCCAATTCG GGATTTTTCT
4101 TGGGAAGTTT CGGGAAGAAA TTGGAATGGA ATAATATAGA TTCATACAGA
4151 GGAAAAGGTT CTCTATTGAT GCAAACGCTG TACCTAGAGG ATAGGGATAG
4201 AGGAAGAGGG AAAAATCGAA ATGAAATAAA TAAGAATAA AGCAAAAAAA
4251 AAATAAGTCG AAGATAGAAG AGCCCAGATT CCAATGAAG AAATGGAAAC
4301 TCGAAAAGGA TCCTTCTGAT TCTCAAAGAA TGAGGGGCAA GGGGATTGAT
4351 ACCGAGAAAG ATTTCTTCTT ATTATAAGAC GTGATTTGAT CCGCATATGT
4401 TTGGTAAAAG AACAATCTTC TCCTTTAATC ATAAATGGAA AGTGTTCAAT
4451 TAGAACATGA AAACGTGACT CAATTGGTCT TAGTTAGTCT TCGGGACGGA
4501 GTGGAAGAAA GGGCGAAGAC TCTCGAACGA GGAAAAGGAT CCCTTCGAAA
4551 GAATTGAACG AGGAGCCGTA TTAGGTGAAA ATCTCATGTA CGATTCTGTA
4601 GAGGGACAGG AAGGGTGACT TATCTGTCTG CTTTCCACT ATCAACCCCA
4651 AAAAACCCAA CTCTGCCTTA C

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aada

Rice Right-targeting sequence

125878

Figure 33B

pMSK49.seq Length: 5263

Figure 34A

122488

1	GGGAACGGAT	TCACCGCCGT	ATGGCTGACC	GGCGATTACT	AGCGATTCCCT
51	GCTTCATGCA	GGCGAGTTGC	AGCCTGCAAT	CCGAAGTGAG	GACGGGTTTT
101	TGGAGTTAGC	TCACCCTCGC	GAGATCGCGA	CCCTTTGTCC	CGCCCATTTG
151	AGCACGTGTG	TCGCCCAGGG	CATAAGGGGC	ATGATGACTT	GGCCTCATCC
201	TCTCCTTCCT	CCGGCTTAAC	ACCGGCGGTC	TGTTCAGGGT	TCCAAACTCA
251	TAGTGGCAAC	TAAACACGAG	GGTTGCGCTC	GTTGCGAGAC	TTAACCCAAC
301	ACCTTACGGC	ACGAGCTGAC	GACAGCCATG	CACCACCTGT	GTCCGCGTTC
351	CCGAGGGCAC	CCCTCTCTTT	CAAGAGGATT	CGCGGCATGT	CAAGCCCTGG
401	TAAGGTTCTT	CGCTTTGCAT	CGAATTAAAC	CACATGCTCC	ACCGCTTGTT
451	CGGGCCCCCG	TCAATTCCTT	TGAGTTTCAT	TCTTGCGAAC	GTACTCCCCA
501	GGCGGGATAC	TTAACGCGTT	AGCTACAGCA	CTGCACGGTT	CGAGTCGCAC
551	AGCACCTAGT	ATCCATCGTT	TACGGCTAGG	ACTACTGGGG	TCTCTAATCC
601	CATTTGCTCC	CCTAGCTTTC	GTCTCTCAGT	GTCACTGTCC	GCCCAGCAGA
651	GTGCTTTTCG	CGTTGGTGTG	CTTTCCGATC	TCAATGCATT	TCACCGCTCC
701	ACCGGAAATT	CCCTCTGCCC	CTACCGTACT	CCAGCTTGGT	AGTTTCCACC
751	GCCTGTCCAG	GGTTGAGCCC	TGGGATTTGA	CGGCGGACTT	GAAAAGCCAC
801	CTACAGACGC	TTTACGCCCC	ATCATTCCGG	ATAACGCTTG	CATCCTCTGT
851	CTTACCGCGG	CTGCTGGCAC	AGAGTTAGCC	GATGCTTATT	CCTCAGATAAC
901	CGTCATTGTT	TCTTCTCCGA	GAAAAGAAGT	TGACGACCCG	TGGGCCTTCC
951	ACCTCCACGC	GGCATTGCTC	GGTCAGGCTT	TCGCCCATTG	CGGAAAATTCC
1001	CCCACTGCTG	CCTCCCGTAG	GAGTCTGGGC	CGTGTCTCAG	TCCCAGTGTG
1051	GCTGATCATC	CTCTCGGACC	AGCTACTGAT	CATCGCCTTG	GTAAGCTATT
1101	GCCTCACCAA	CTAGCTAATC	AGACGCGAGC	CCCTCCTTGG	GCGGATTTCT
1151	CCTTTTGCTC	CTCAGCCTAC	GGGGTATTAG	CAACCGTTTC	CAGTTGTTGT
1201	TCCCTTCCCA	AGGGCAGGTT	CTTACGCGTT	ACTCACCCTG	TCGCCACTGG
1251	AAACACCACT	TCCCGTTCTGA	CTTGCATGTG	TTAAGCATGC	CGCCAGCGTT
1301	CATCCTGAGC	CAGGATCGAA	CTCTCCATGA	GATTCAATAGT	TGCATTACTT
1351	TAGCTTCTCT	TATTCCTAGA	CAAAGCGGAT	TCGGAATTGT	CTTTCCTTCC
1401	AAGGATAAAT	TGTATCCATG	CGTTTCAGAT	TATTAGCCTG	GAGTTCGCCA
1451	CCAGCAGTAT	AGCCAAACCCT	ACCCTATCAC	GTCAATCCCA	CAAGCCTCTT
1501	ATCCATTCCC	GTTTCGATCGT	GGCGGGGGGA	GTAAGTCAAA	ATAGAAAAAA
1551	CTCACATTGG	GTTTAGGGAT	AATCAGGCTC	GAAGTATGA	CTTCCACCAC
1601	GTCAAGGTGA	CACTCTACCG	CTGAGTTATA	TCCCTTCCCC	GTCCCCTCGA
1651	GAAAGAGAAT	TACCGAATCC	TAAGGCAAAAG	GGGCGAGAAA	CTCAAGGCCA
1701	CCCTTCCTCC	GGGCTTTCTT	TCCACACTAT	TATGGATAGT	CAAATAATGG
1751	GAAAATTGG	ATTCAATTGT	CAACCGGTCC	TATCGAAAAT	AGGATTGACT
1801	ATGGATTCTG	GCCATAGCAC	ATGGTTTCAT	AAAATCTGTA	CGATTTTCCC
1851	GATCTAAATC	GAGCAGSTTT	CCATGAAGAA	gatcgacggt	atcgataagc
1901	TTTCTAGAAAT	AAATGCAAGA	AAATAACCTC	TCCTTCTTTT	TCTATAATGT
1951	AAACAAAAAA	GTCTATGTAA	GTAAAATACT	AGTAAATAAA	TAAAAAGAAA
2001	AAAAGAAAGG	AGCAATAGCA	COCTCTTGAT	AGAACAAGAA	AATGATTATT
2051	GCTCCTTTCT	TTTCAABACC	TCCTATAGAC	TAGGCCAGGA	TCgctctaga
2101	gccttattttg	TATAGTTCAT	CCATGCCATG	TGTAATCCCA	GCAGCTGTTA
2151	CAAACCTCAAG	AAGGACCATG	TGGTCTCTCT	TTTCGTTGGG	ATCTTTTCGAA
2201	AGGGCAGATT	GTGTGGACAG	GTAATGGTTG	TCTGGTAAAA	GGACAGGGCC
2251	ATCGCCAATT	GGAGTATTTT	GTTGATAATG	GTCTGCTAGT	TGAACGCTTC
2301	CATCTTCAAT	GTTGTGTCTA	ATTTTGAAGT	TAGCTTTGAT	TCCATTCTTT
2351	TGTTTGTCTG	CCGTGATGTA	TACGTTGTGG	GAGTTGTAGT	TGTATTCCAA
2401	CTTGTGGCCG	AGGATGTTTC	CGTCCTCCTT	GAAATCGATT	CCCTTAAGCT
2451	CGATCCTGTT	GACGAGGGTG	TCTCCCTCAA	ACTTGACTTC	AGCACGTGTC
2501	TTGTAGTTCC	CGTCGTCTCT	GAAAGAGATG	GTCCTCTCCT	GCACGTATCC
2551	CTCAGGCATG	GCGCTCTTGA	AGAAGTCGTG	CCGCTTCATA	TGATCTGGGT
2601	ATCTTGAAAA	GCATTGAACA	CCATAAGAGA	AAGTAGTGAC	AAGTGTGGCC
2651	CAAGGAACAG	GTAGTTTTC	AGTAGTGCAA	ATAAATTTAA	GGGTAAGTTT
2701	TCCGTATGTT	GCATCACCTT	CACCTCTCC	ACTGACAGAA	AATTTGTGCC

Rice left targeting Sequence

1756A

JFP

Figure 34B

pMSK49.seq Length: 5263

2751 CATTAAACATC ACCATCTAAT TCAACAAGAA TTGGGACAAC TCCAGTGAAA
 2801 AGTTCTTCTC CTTTACTagc CATggcgacc tccaattttc cttcaactgc
 2851 aagttcTTTG CCACTACCT TGGTGATCTC GCCTTTCACG TAGTGGACAA
 2901 ATTCTTCCAA CTGATCTGCG CGCGAGGCCA AGCGATCTTC TTCTTGTCCTA
 2951 AGATAAGCCT GTCTAGCTTC AAGTATGACG GGCTGATACT GGGCCGGCAG
 3001 GCGCTCCATT GCCCAGTCGG CAGCGACATC CTTCCGGCGCG ATTTTGCCCG
 3051 TTAGTGGCGCT GTACCAATG CGGGACAACG TAAGCACTAC ATTTGCGCTCA
 3101 TCGCCAGCCC AGTCGGGGCGG CGAGTTCCAT AGCGTTAAGG TTTCATTTAG
 3151 CGCCTCAAAT AGATCCTGTT CAGGAACCGG ATCAAAGAGT TCCTCCGCGG
 3201 CIGGACCTAC CAAGGCAACG CTATGTTCTC TTGCTTTTGT CAGCAAGATA
 3251 GCCAGATCAA TGTCGATCGT GGCTGGCTCG AAGATACCTG CAAGAATGTC
 3301 ATTGCGCTGC CATCTCCTAA ATTGCAGTTC GCGCTTAGCT GGATAACGCC
 3351 ACGGAATGAT GTCGTCTGTC ACAACAATGG TGACTTCTAC AGCGCGGAGA
 3401 ATCTCGCTCT CTCCAGGGGA AGCCGAAGTT TCCAAAAGGT CGTTGATCAA
 3451 AGCTCGCCGC GTTGTTCAT CAAGCCTTAC GGTCACCGTA ACCAGCAAT
 3501 CAATATCACT GTGTGGCTTC AGGCCGCCAT CCACTGCGGA GCGTACAAN
 3551 TGACGGCCA GCAACGTCGG TTCGAGATGG CGCTCGATGA CGCCAACCTAC
 3601 CTCTGATAGT TGAGTCGATA CTTCCGGCGAT CACCGCTTCg ctaggcaagt
 3651 cttcttcaga aatgagtttt tgttcgctag cTGTCCACC AGTCATGCTT
 3701 GCCATATGTA TATCTCCTTC TTAAGTTAA ACAAATTAT TTCTAGtGGG
 3751 AAACCGTTGT GGTCTCCCTC CCAGAAATAT AGCCATCCCT GCCCCTCAC
 3801 GTCAATCCCA CGAGCCTCTT ATCCATTCTC ATTGAACGAC GCGGGGGGAG
 3851 Cgagctcgaa ttcctgcagc ccatcTTAC CATTTCGGAA GGAAGTGGGG
 3901 CTACATTTCT TTTCAATTTT CATTCAAGAG TTTCTTATCT GTTCCACGC
 3951 CCTTTTTTGA GACCTCGAAA CATGAAATGG ACAAATTCCT TCTCTTAGGA
 4001 ACACATACAA GAAAAAGGAT AATGGTAGCC CTCCCATTA CTACTTCATT
 4051 TCATTTATGA ATTTATAGT AATAGAAATC CATGTCCTAC CGAGACAGAA
 4101 TTTCGAACTT GCTATCCTCT TGCCTAATAG GCAAAGATTG ACCTCTGTAG
 4151 AAAGAATGAT TCATTCCGAT CGATATGAGG ACCCAACTAC GTTGCAATTGC
 4201 AGAATCCATG TTCCATATTT GAAGAGGGTT GACCTCTGTG CTCTCTCAT
 4251 GGTACAATCC TCTTCTGCT GAGCCCCCTT TCTCTCGGT CCACAGAGAA
 4301 AAAATGGAGG ACTGGTGCCG ACAGTTCATC ACGGAAGAAA GAACTCACAG
 4351 AGCCGGGATC GCTAACTAAT AGAATAGTAC TACTAATAA TACTAATATA
 4401 TAGAAATAGA TATctagcta GAAATAGAAA CAACTAATAT ATAGATAATC
 4451 GAAATTGAAA AGAAGTGTCT TTTCTGTATA CTTTCCCCST TCTATTGCTA
 4501 CCGCGGGTCT TATGCAATCG ATCGGATCAT ATAGATATCC CTTCAACACA
 4551 ACATAGGTCA TCGAAAGGAT CTCGGACGAC TCACCAAAGC ACGAAAGCCA
 4601 GTTAGAAAAT GGATTCTAT TTGAAGAGTG CCTAACCAGC TGGATAAGCT
 4651 CACATTAACC CGTCAATTTT GGATCCAATT CGGGATTTT CTTGGGAAGT
 4701 TTCGGGAAGA AATTGGAATG GAATAATATA GATTCAATCA GAGGAAAAGG
 4751 TTCTCTATTG ATGCAAACGC TGTACCTAGA GGATAGGGAT AGAGGAAGAG
 4801 GGAAAAATCG AATGAAATA AATAAAGAA AAAGCAAAA AAAAATAAGT
 4851 CGAAGATAGA AGAGCCAGA TTCCAAATGA AGAAATGGAA ACTCGAAAAG
 4901 GATCCTTCTG ATTCTCAAAG AATGAGGGGC AAGGGGATTG ATACCGAGAA
 4951 AGATTTCTTC TTATTATAAG ACGTGATTG ATCCGCATAT GTTTGGTAAA
 5001 AGAACAATCT TCTCCTTTAA TCATAAATGG AAAGTGTTCA ATTAGAACAT
 5051 GAAAACGTGA CTCAATTGGT CTTAGTTAGT CTTCCGGGACG GAGTGAAGA
 5101 AAGGGCGAAG ACTCTCGAAC GAGGAAAAGG ATCCCTTCGA AAGAATTGAA
 5151 CGAGGAGCCG TATTAGGTGA AAATCTCATG TACGATTCTG TAGAGGGACA
 5201 GGAAGGGTGA CTTATCTGTC GACTTTTCCA CTATCAACCC CAAAAAACC
 5251 AACTCTGCCT TAG

sada

L79108

Rice Right targeting sequence

125878

Gene	Product	Plasmid
<i>aadA16gfp</i>	FLARE16-S	pMSK51 (BS)
<i>aadA16gfp-S1</i>	FLARE16-S1	pMSK56 (Nt-pRV111B)
<i>aadA16gfp-S2</i>	FLARE16-S2	pMSK57 (Nt-pRV111B)
<i>aadA11gfp-S3</i>	FLARE11-S3	pMSK49 (Os-pMSK49)

Figure 35